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OM nucleic - nucleic search, using sw model

Run on: June 8, 2003, 23:36:29 ; Search time 211 Seconds
(without alignments)
9073.778 Million cell updates/sec

Title: US-09-899-422A-1

Perfect score: 1368

Sequence: 1 atgggcctctccaccgtgcc.....cgcacagttctctcagatga 1368

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications, NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|---------------------|
| 1 | 1368 | 100.0 | 1368 | 9 | US-09-898-234-1 |
| 2 | 1368 | 100.0 | 1368 | 9 | US-09-899-429A-1 |
| 3 | 1368 | 100.0 | 1368 | 9 | US-09-792-356-1 |
| 4 | 1368 | 100.0 | 1368 | 10 | US-09-899-422-1 |
| 5 | 1368 | 100.0 | 2141 | 9 | US-09-898-234-16 |
| 6 | 1368 | 100.0 | 2141 | 9 | US-09-899-429A-26 |
| 7 | 1368 | 100.0 | 2141 | 9 | US-09-792-356-16 |
| 8 | 1368 | 100.0 | 2141 | 10 | US-09-899-422-16 |
| 9 | 1366.4 | 99.9 | 2111 | 10 | US-09-880-107-2360 |
| 10 | 1366.4 | 99.9 | 2175 | 12 | US-10-120-397-1 |
| 11 | 1363.2 | 99.6 | 1368 | 9 | US-10-252-408-3 |
| 12 | 1122 | 82.0 | 1334 | 9 | US-09-898-234-11 |
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| 15 | 1117.2 | 81.7 | 1334 | 9 | US-09-899-429A-21 |
| 16 | 743.4 | 54.3 | 2130 | 10 | US-09-917-800A-1601 |
| 17 | 735.4 | 53.8 | 2173 | 9 | US-09-898-234-14 |
| 18 | 735.4 | 53.8 | 2173 | 9 | US-09-899-429A-24 |
| 19 | 735.4 | 53.8 | 2173 | 9 | US-09-792-356-14 |

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| 20 | 735.4 | 53.8 | 2173 | 10 | US-09-899-422-14 | Sequence 14, Appl |
| 21 | 685.4 | 50.1 | 2440 | 10 | US-09-970-532-1 | Sequence 1, Appl |
| 22 | 633 | 46.3 | 633 | 9 | US-09-899-429A-7 | Sequence 7, Appl |
| 23 | 603 | 44.1 | 603 | 9 | US-09-899-429A-13 | Sequence 13, Appl |
| 24 | 557 | 40.7 | 600 | 9 | US-09-899-429A-11 | Sequence 11, Appl |
| 25 | 546 | 39.9 | 549 | 9 | US-09-899-429A-9 | Sequence 9, Appl |
| 26 | 527 | 38.5 | 570 | 9 | US-09-899-429A-17 | Sequence 17, Appl |
| 27 | 516 | 37.7 | 519 | 9 | US-09-899-429A-15 | Sequence 15, Appl |
| 28 | 514 | 37.6 | 1301 | 10 | US-09-756-186-7 | Sequence 7, Appl |
| 29 | 513 | 37.5 | 516 | 9 | US-09-899-429A-19 | Sequence 19, Appl |
| 30 | 506 | 37.0 | 1147 | 10 | US-09-756-186-5 | Sequence 5, Appl |
| 31 | 483 | 35.3 | 483 | 9 | US-09-898-234-3 | Sequence 3, Appl |
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| 33 | 483 | 35.3 | 483 | 9 | US-09-792-356-3 | Sequence 3, Appl |
| 34 | 483 | 35.3 | 483 | 9 | US-09-882-735-1 | Sequence 1, Appl |
| 35 | 483 | 35.3 | 483 | 10 | US-09-899-422-3 | Sequence 3, Appl |
| 36 | 483 | 35.3 | 483 | 10 | US-09-907-263-1 | Sequence 1, Appl |
| 37 | 483 | 35.3 | 486 | 9 | US-09-899-429A-5 | Sequence 5, Appl |
| 38 | 479 | 35.0 | 479 | 9 | US-10-043-487-100 | Sequence 100, App |
| 39 | 467 | 34.1 | 1674 | 9 | US-09-359-595-12 | Sequence 12, Appl |
| 40 | 424.4 | 31.0 | 1049 | 10 | US-09-756-186-1 | Sequence 1, Appl |
| 41 | 424.4 | 31.0 | 1202 | 10 | US-09-756-186-3 | Sequence 3, Appl |
| 42 | 375.8 | 27.5 | 507 | 9 | US-09-911-904-129 | Sequence 129, App |
| 43 | 337 | 24.6 | 427 | 10 | US-09-876-889-236 | Sequence 236, App |
| 44 | 330 | 24.1 | 543 | 10 | US-09-970-532-3 | Sequence 3, Appl |
| 45 | 329.6 | 24.1 | 5870 | 10 | US-09-838-718A-8 | Sequence 8, Appl |

ALIGNMENTS

RESULT 1

US-09-898-234-1
; Sequence 1, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-1
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 09/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1368)
; NAME/KEY: sig_peptide
; LOCATION: (1)..(87)
; NAME/KEY: misc_feature
; LOCATION: (88)..(120)
; OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
; NAME/KEY: misc_feature
; LOCATION: (606)..(633)
; OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by

; OTHER INFORMATION: extracellular proteases following secretion.
US-09-898-234-1

Query Match 100.0%; Score 1368; DB 9; Length 1368;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 901 CCCGGTGACTGTCCCAACTTTGGGCTCCCGCAGAGAGTGGACCAACCTATCAGGG 960
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RESULT 2
US-09-899-429A-1
; Sequence 1, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
; NAME/KEY: sig_peptide
; LOCATION: (1)..(87)
; NAME/KEY: misc_feature
; LOCATION: (88)..(120)
; OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
; OTHER INFORMATION: extracellular proteases following secretion
; NAME/KEY: misc_feature
; LOCATION: (606)..(633)
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; OTHER INFORMATION: extracellular proteases following secretion
US-09-899-429A-1


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RESULT 8

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US-09-899-422-16
; Sequence 16, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratos, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98,385-H
; CURRENT APPLICATION NUMBER: US/09/899,422
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
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; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2141
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (213)..(1580)
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
; OTHER INFORMATION: ITNF-R2
US-09-899-422-16
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GGAATATACCCCTCAGGGTTATTGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 273 GGAATATACCCCTCAGGGTTATTGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 332
QY 121 CATAGTGTGCTGCCCAAGGAAATATATCCACCTCAAAATATATCCATTTGCTGTACC 180
Db 333 CATAGTGTGCTGCCCAAGGAAATATATCCACCTCAAAATATATCCATTTGCTGTACC 392
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QY 241 TGCAGGAGTGTGAGAGGGCTCTTCCACCTTCCAGAAACCTCAGAAACCTCAGAAACCTCAGAAACCTC 300
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QY 301 AGCTGCTCCAAATGCCAAAGGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
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QY 361 CGGACACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 573 CGGACACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 632
QY 421 TTCCAGTGTTCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
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QY 601 AATCTTAAGGCACTGAGGACTCAGGACCAACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
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QY 661 GGTCTTTGCCCTTTTATCCCTCCTCTCTCATTTGTTTAAATGATCGTACCAACGGTGAAG 720
Db 873 GGTCTTTGCCCTTTTATCCCTCCTCTCTCATTTGTTTAAATGATCGTACCAACGGTGAAG 932
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Db 933 TCCAAAGCTCTACTCCCAATGTTTGTGGAAATGACACCTGTAAAGAGGGGAGCTGAA 992
Qy 781 GGAACCTACTACTAAGCCCTTGGCCCAAGCCCAAGCTTCACTCCCACTCCAGGCTTCACC 840
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Qy 841 CCACACCTTGGGCTTCACTAGTCCGCTGCGCAGTTCACCTTCCAGCTCCACCTATACC 900
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RESULT 9

US-09-880-107-2360
; Sequence 2360, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2360
; LENGTH: 2111
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M58286
US-09-880-107-2360

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Best Local Similarity 99.99; Pred. No. 0;

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Db 727 TCCTGTAGTAACGTAAAGAAAGCTGAGTGCAGGAGTGTGCTGCTGCTGCTGCTGCTGCTG 786
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Job time : 214 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2003, 01:14:14 ; Search time 81 Seconds
(without alignments)
1722.690 Million cell updates/sec

Title: US-09-899-422A-2

Perfect score: 2487

Sequence: 1 MGLSVPLLLPLVLELLVDIEEALCPAALPPAPSLLR 455

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 2487 | 100.0 | 2161 | 4 | US-09-505-250-3 |
| 3 | 2487 | 100.0 | 2175 | 1 | US-08-321-668-1 |
| 4 | 2487 | 100.0 | 2175 | 1 | US-08-837-941-1 |
| 5 | 2487 | 100.0 | 2175 | 1 | US-08-126-016-1 |
| 6 | 2487 | 100.0 | 2175 | 1 | US-08-054-970-1 |
| 7 | 2482 | 99.8 | 2062 | 1 | US-08-050-319B-24 |
| 8 | 2482 | 99.8 | 2062 | 2 | US-08-465-982-24 |
| 9 | 1521 | 61.2 | 1956 | 2 | US-08-762-308-10 |
| 10 | 1517 | 61.0 | 2440 | 1 | US-09-513-007-1 |
| 11 | 1223.5 | 49.2 | 6889 | 1 | US-08-286-740-2 |
| 12 | 1223.5 | 49.2 | 6889 | 5 | PCR-US95-09576-2 |

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| 13 | 1192 | 47.9 | 6896 | 2 | US-08-627-151A-6 | Sequence 6, Appl |
| 14 | 1124 | 45.2 | 600 | 1 | US-08-050-319B-47 | Sequence 47, Appl |
| 15 | 1124 | 45.2 | 600 | 1 | US-08-465-982-47 | Sequence 47, Appl |
| 16 | 1016 | 40.9 | 1301 | 4 | US-08-804-166-7 | Sequence 7, Appl |
| 17 | 1016 | 40.9 | 1301 | 4 | US-08-910-991-7 | Sequence 7, Appl |
| 18 | 995.5 | 40.0 | 1147 | 4 | US-08-804-166-5 | Sequence 5, Appl |
| 19 | 995.5 | 40.0 | 1147 | 4 | US-08-910-991-5 | Sequence 5, Appl |
| 20 | 992 | 39.9 | 1478 | 4 | US-09-149-922-6 | Sequence 6, Appl |
| 21 | 946 | 38.0 | 501 | 1 | US-08-050-319B-1 | Sequence 1, Appl |
| 22 | 946 | 38.0 | 501 | 1 | US-08-465-982-1 | Sequence 1, Appl |
| 23 | 946 | 38.0 | 504 | 1 | US-08-050-319B-56 | Sequence 56, Appl |
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| 25 | 941 | 37.8 | 483 | 4 | US-09-326-394-1 | Sequence 1, Appl |
| 26 | 870.5 | 35.0 | 1202 | 4 | US-08-804-166-3 | Sequence 3, Appl |
| 27 | 870.5 | 35.0 | 1202 | 4 | US-08-910-991-3 | Sequence 3, Appl |
| 28 | 854.5 | 34.4 | 477 | 2 | US-08-050-319B-53 | Sequence 53, Appl |
| 29 | 854.5 | 34.4 | 477 | 2 | US-08-465-982-53 | Sequence 53, Appl |
| 30 | 852 | 34.3 | 1049 | 4 | US-08-804-166-1 | Sequence 1, Appl |
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| 34 | 840 | 33.8 | 474 | 1 | US-08-050-319B-49 | Sequence 49, Appl |
| 35 | 840 | 33.8 | 474 | 2 | US-08-465-982-49 | Sequence 49, Appl |
| 36 | 738.5 | 29.7 | 543 | 4 | US-09-513-007-3 | Sequence 3, Appl |
| 37 | 731 | 29.4 | 372 | 1 | US-08-050-319B-3 | Sequence 3, Appl |
| 38 | 731 | 29.4 | 372 | 2 | US-08-465-982-3 | Sequence 3, Appl |
| 39 | 582 | 23.4 | 427 | 4 | US-09-397-787-236 | Sequence 236, App |
| 40 | 395.5 | 15.9 | 1783 | 3 | US-08-815-469-1 | Sequence 1, Appl |
| 41 | 387 | 15.6 | 1634 | 4 | US-08-928-069-11 | Sequence 11, Appl |
| 42 | 387 | 15.6 | 1634 | 4 | US-08-828-683A-9 | Sequence 9, Appl |
| 43 | 378 | 15.2 | 1254 | 3 | US-08-815-469-3 | Sequence 3, Appl |
| 44 | 246 | 9.9 | 1600 | 3 | US-08-602-791-1 | Sequence 1, Appl |
| 45 | 246 | 9.9 | 3386 | 4 | US-09-041-886-1 | Sequence 1, Appl |

ALIGNMENTS

RESULT 1
US-09-106-038A-1
; Sequence 1, Application US/09106038A
; Patent No. 6007995
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker and Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Isis Pharmaceuticals, Inc.
; STREET: 2292 Faraday Avenue
; CITY: Carlsbad
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92008
; COMPUTER READABLE FORM:
; Sequence 1, 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,038A
; FILING DATE: June 26, 1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Laurel Spear Bernstein
; REGISTRATION NUMBER: 37,280
; REFERENCE/DOCKET NUMBER: RTS-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (760) 931-9200
; TELEFAX: (760) 603-3820
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161
; TYPE: nucleic acid

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QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
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QY 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
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QY 221 GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
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QY 261 GlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
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QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr 300
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RESULT 3
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; Sequence 1, Application US/08321668
; Patent No. 5665859
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; APPLICANT: VARPOLOMEEV, Eugene
; APPLICANT: BATKIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSER: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/321,668
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107268
; FILING DATE: 12-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2175 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1620
; US-08-321-668-1

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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; STRANDEDNESS: single
; TOPOLOGY: linear
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; NAME/KEY: CDS
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; LOCATION: 319..1620
US-08-126-016-1

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Alignment Scores:

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Score: 2487.00 Matches: 455
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Db 796 TCCGTAGTAACCTGTAAGAAAGCCTGGAGTGCACGAAGTGTGCTACCCACAGATTGAG 855
Qy 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
Db 856 AATGTTAAGGCACTGAGGACTAGGACCAACACAGTGTGTGCCCCCTGGTCATTTCTTTT 915
Qy 221 GlyLeuCysLeuLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTyrLys 240
Db 916 GGTCTTTGGCTTTATCCCTCTCTTCATTTGGTTATATGATATCGCTACCAACAGGTGGAAG 975
Qy 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyLeuGlu 260
Db 976 TCCAAGCTCTACTCCTATTGTTGGGAAATCGACACCTGAAAGAGGGGGAGCTTGAA 1035

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Qy 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
Db 1036 GGAAGTACTACTAAGCCCTTGGCCCCAAACCAAGCTTCACTCCCACTCCAGGCTTCAAC 1095
Qy 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrThr 300
Db 1096 CCCACCTTGGGCTTTCAGTCCCGCTCCAGCTTCCACCTTCACTCCAGCTTCACTATACC 1155
Qy 301 ProGlyAspCysProAsnProAlaProArgGluValAlaProProTyrGlnGly 320
Db 1156 CCCGCTGACTGTCCCAACTTTCGCGCTCCCGCAGAGAGGTGGCCACCCATATCAGGG 1215
Qy 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
Db 1216 GCTGACCCCTCTCTGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAAGAG 1275
Qy 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
Db 1276 TGGAGGACAGCGCCCAAGCCACAGAGCTAGACACTGATGACCCCGCAGCGCTGTAC 1335
Qy 361 AlaValValGluAsnValProProLeuArgTyrLysGluPheValArgAlaGluLeu 380
Db 1336 GCCGTGTGGAGAACGTGCCCGCTTGGCTGGAGAGATTCGTGCGGCGCTAGGCGTG 1395
Qy 381 SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
Db 1396 AGCACCACAGATCGATCGCTGGAGTGCAGAACGGGCGCTGCTGCGGAGCGCAA 1455
Qy 401 TyrSerMetLeuAlaThrTrpArgArgThrProArgArgGluAlaThrLeuGluLeu 420
Db 1456 TACAGCATGTGGCGACCTGGAGCGCGCACCGCGCGGCGGAGCGACGCTGAGCTG 1515
Qy 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAla 440
Db 1516 CTGGAGCGCTGCTCCGCGACATGGACTGCTGGGCTGCTTGGAGAGACATCGAGAGCGG 1575
Qy 441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
Db 1576 CTTTGGCGCGCGCGCGCTCCCGCGCGCGCGAGTCTTCTCAGA 1620

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RESULT 6

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US-08-054-970-1
; Sequence 1, Application US/08054970
; Patent No. 6395267
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/054,970
; FILING DATE: 03-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633

```

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2175 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 256..1620

; US-08-054-970-1

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 3,12e-229 | Length: | 2175 |
| Score: | 2487.00 | Matches: | 455 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 4 | Gaps: | 0 |

US-09-899-422a-2 (1-455) x US-08-054-970-1 (1-2175)

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QY      1 MetGlyLeuSerThrValProAspLeuLeuValProLeuValLeuLeuLeuVal 20
DB      256 ATGGGCGCTCTCCACCGTGGCTGACCTGCTGCTGCGCTGGTCTCTCTGGAGCTGTGGTG 315

QY      21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
DB      316 GGAATATACCCCTCAGGGGTTATTGGACTGTGTCCTCACCTAGGGGACAGGGGAGAAGA 375

QY      41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysThr 60
DB      376 GATAGTGTGTGTCCTCAAGGAAATATATCCACCTCCAAATTAATTCGATTTCGTGTACC 435

QY      61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
DB      436 AAGTCCACCAAGAAACCTACTTGTACATGACTGTCCAGGCGCGGGCAGGATACGGAC 495

QY      81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
DB      496 TGCAGGGAGTGTGAGAGCGGCTCTCCCTCAATGGGACCGCTCACCAACACCTCAGACACTGCCTC 555

QY      101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
DB      556 AGCTGCTCCAAATGCGGAAAGAAATGGTCAAGTGGAGATCTCTTTCACACTGGAC 615

QY      121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
DB      616 CGGGACCGCTGTGGCTGCAGGAGAACCACTACCGGCATTTGGAGTCAAAACCTT 675

QY      141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
DB      676 TTCCAGTGTCTCAATTCAGCCCTCGCTCAATGGGACCGCTCACCTCTCTCTGCCAGGAG 735

QY      161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
DB      736 AAACAGAACCCGTGTGACCTGCCATGCAGGTTCCTTCTAAGAGAAACAGTGTGTC 795

QY      181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
DB      796 TCCTGTAGTAAGTAAAGAAACCTGGAGTGCACGAGTGTGCTACCCAGATGTAG 855

QY      201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
DB      856 AATGTTAAGGGCACTGAGGACTCAGGACACACAGTGTCTGTCCTGCTGCTATTTCTTT 915

QY      221 GlyLeuCysLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
DB      916 GGTCTTTGCTTTTATCCCTCTCTCTCAATGTTTAAATGATATCGGTACCAACGGTGGAG 975

QY      241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGluLeuGlu 260
DB      976 TCCAGACTCTACTCCATGTTTGTGGGAAATCGACACCTCAAAAGAGGGGAGCTTGAA 1035

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QY      261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
DB      1036 GGAAGTACTACTAAGCCCTGGCCCAACCAAGCTTCAGTCCACTCCAGGCTTCCACC 1095

QY      281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrThr 300
DB      1096 CCCACCTGGGCTTCAGTCCCTGGCCAGTTCACCTTCACCTCCAGCTCCACCTATAC 1155

QY      301 ProGlyAspCysProAsnPheAlaAlaProArgGluValAlaProProTyrGlnGly 320
DB      1156 CCCGGTACTGTCCCAACTTTGGGCTCCCGCAGAGAGTGGCACCACCTATACAGGG 1215

QY      321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
DB      1216 GCTGACCCCATCTTGGCAGACGCTCGCTCGACCCCATCCCAACCCCTTTCAGAG 1275

QY      341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
DB      1276 TGGGAGGACAGCGCCCAAGCCACAGACCTAGACACTGATGACCCCGCAGCTGTAC 1335

QY      361 AlaValValGluAsnValProProLeuArgTyrLysGluPheValArgLeuGlyLeu 380
DB      1336 GCGGTGGTGGAACGTCGCCCTGCTGGAGGAATTCGTGGCGGCTTAGGGCTG 1395

QY      381 SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
DB      1396 AGCGACACAGATGATCGGTGGAGTGCAGACGGGCGCTGCTGCGCGAGGCGCAA 1455

QY      401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420
DB      1456 TACAGCATCTGGCGACCTGGAGGGCGGCACCGCGCGGAGGCCACGCTGGAGCTG 1515

QY      421 LeuGlyArgValLeuArgAspMetAspLeuGlyCysLeuGluAspIleGluAla 440
DB      1516 CTGGGACGGTGTCTCGCGCACATGACCTGCTGGGCTGCTGGAGACATCGAGGAGCG 1575

QY      441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
DB      1576 CTTTGGCGCGCGCGCTCCCGCGCGCGCGCAGTCTTCTCAGA 1620

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RESULT 7

US-08-050-319B-24

; Sequence 24, Application US/08050319B

; Patent No. 5633145

; GENERAL INFORMATION:

; APPLICANT: M. Feldmann, P.W. Gray,

; APPLICANT: M.J.C. Turner, F.M. Brennan

; TITLE OF INVENTION: Modified human TNFalpha (Tumor

; TITLE OF INVENTION: Necrosis factor alpha) Receptor

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Reed & Robbins

; STREET: 635 Bryant Street

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/050,319B

; FILING DATE: 10-May-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Robbins, Roberta L.

; REGISTRATION NUMBER: 33,208

; REFERENCE/DOCKET NUMBER: 5150-0030

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 617-8999

| | | |
|--|---|------|
| 815 | GGTCTTTGGCTTTATATCCCTCTCTTCATATGGTTTAAATGATATCGTACCAACCGTGAAG | 874 |
| 241 | SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu | 260 |
| 875 | TCCAAGCTCTACTCCATTTGTTGGGAATCGACACCTGAAAAGAGGGGGAGCTTGA | 934 |
| 261 | GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr | 280 |
| 935 | GGAACTACTACTAAGCCCTGGCCCAAAACCCAAAGCTTCAGTCCCACTCCAGGCTTCACC | 994 |
| 281 | ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrThrThr | 300 |
| 995 | CCACCCCTGGCTTCAGTCCGTCGCGCAGTTCACCTTCACCTCCAGCTCCACCTATACC | 1054 |
| 301 | ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly | 320 |
| 1055 | CCCGGTGACTGTCCCAACITTTGGGGCTCCCGCGAGAGAGTGGCACCACCTATCAGGGG | 1114 |
| 321 | AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys | 340 |
| 1115 | GCTGACCCCATCTTGGCAGACGCGCTCGCTCGGACCCCATCCCAACCCCTTCAGAAG | 1174 |
| 341 | TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr | 360 |
| 1175 | TGGGAGGACAGTGCACAAAGCCACAGAGCCTAGACACTGATGACCCCGGACGCTGTAC | 1234 |
| 361 | AlaValValGluAsnValProProLeuArgTriPlysGluPheValArgArgLeuGlyLeu | 380 |
| 1235 | GCGTGGTGAGAACGTGCCCGGTGGCGTGGAGGATTCGTGGCGGCCCTAGGGCTG | 1294 |
| 381 | SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln | 400 |
| 1295 | AGCGACCACGAGATCGATCGCTGGAGCTCAGAACGGGGCGCTGCCTGCGGAGGCGCAA | 1354 |
| 401 | TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu | 420 |
| 1355 | TACAGCATGCTGGCAGCTGGAGCGCGGCACCGCGCGGCGGAGCCACGCTGGAGCTG | 1414 |
| 421 | LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAla | 440 |
| 1415 | CTGGGACGGTGTCTCGCGACATGGACCTGCTGGGCTGCTGGAGGACATCGAGGAGCGG | 1474 |
| 441 | LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg | 455 |
| 1475 | CTTTGGCGCCCGCGCGCTCCCGCGCGCCAGTCTTCTCAGA | 1519 |
| RESULT 9 | | |
| US-08-762-308-10 | | |
| ; Sequence 10, Application US/08762308 | | |
| ; Patent No. 5925548 | | |
| ; GENERAL INFORMATION: | | |
| ; APPLICANT: Beutler, Bruce A. | | |
| ; APPLICANT: Bazoni, Flavio M. | | |
| ; TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY | | |
| ; TITLE OF INVENTION: SIGNAL | | |
| ; NUMBER OF SEQUENCES: 11 | | |
| ; CORRESPONDENCE ADDRESS: | | |
| ; ADDRESSEE: Arnold, White & Durkee | | |
| ; STREET: P.O. Box 4433 | | |
| ; CITY: Houston | | |
| ; STATE: TX | | |
| ; COUNTRY: USA | | |
| ; ZIP: 77210-4433 | | |
| ; COMPUTER READABLE FORM: | | |
| ; MEDIUM TYPE: Floppy disk | | |
| ; COMPUTER: IBM PC compatible | | |
| ; OPERATING SYSTEM: PC-DOS/MS-DOS | | |
| ; SOFTWARE: PatentIn Release #1.0, Version #1.30 | | |
| ; CURRENT APPLICATION DATA: | | |
| ; APPLICATION NUMBER: US/08/762,308 | | |
| ; FILING DATE: 09-DEC-1996 | | |
| ; CLASSIFICATION: 530 | | |
| ; PRIOR APPLICATION DATA: | | |


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; APPLICATION NUMBER: US 08/224,593
; FILING DATE: 05-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSD:335--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 418-3000
; TELEFAX: 474-7577
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1956 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-762-308-10

Alignment Scores:
Pred. No.:      1,8e+136      Length:      1956
Score:          1321.00       Matches:      294
Percent Similarity: 75.61%    Conservative:  47
Best Local Similarity: 65.19% Mismatches:   98
Query Match:      61.16%     Indels:      12
DB:               2         Gaps:         7

US-09-899-422A-2 (1-455) x US-08-762-308-10 (1-1956)

QY      1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuGluLeuVal 20
        |||||
Ddb     96 ATGGGTCTCCACCACCGTGCCTGGCCTGCTGCTCACTGGTGCTCTGGCTCTGCTGATG 155
QY      21 GlyIleTyrrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
        |||||
Ddb     156 GGGATACATTCATCATCGAGGGTCACTGGACTAGTCCCTTCTTTGGTGACCGGGAGAAGAGG 215
QY      41 AspSerValCyapProGlnGlyLysTyrrIleHisProGlnAsnAsnSerIleCysCysThr 60
        |||||
Ddb     216 GATAGCTTGTGCCCAAGGAAGTAGTCCATTCTTAAGAACAAATTCATCTCTGCTGCACC 275
QY      61 LysCysHisLysGlyThrTyrrLeutyrrAsnAspCyapProGlyProGlyGlnAspThrAsp 80
        |||||
Ddb     276 AAGTGCCACAAGGAACCTACTTGGTGAGTGACTGCCAGCCAGCGGGGGATACAGTC 335
QY      81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
        |||||
Ddb     336 TCACGGGAGTGTGAAGAGGACCTTTACGGCTTCCCAGAAATTCCTTCAGGCAGTGTGCTC 395
QY      101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
        |||||
Ddb     396 ACTTCCAAGACATGTCGGAAGAAATGTCCCAGGTGGAGATCTCTCTTCCCAAGCTGAC 455
QY      121 ArgAspThrValCyeglyCysArgLysAsnGlnTyrrArgHisTyrrTrpSerGluAsnLeu 140
        |||||
Ddb     456 AAGGACACGCTGTGTGGCTGTGAAGGAGAACACAGTTCACACGCTACCTCGAGTGAACAC 515
QY      141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
        |||||
Ddb     516 TTCCAGTGGTGAGTGCAGCCCCCTGCTTCACGGCACCGGTGACAATCCCTCTGATAGGAG 575
QY      161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
        |||||
Ddb     576 ACTCAGAACACCGTGTGTAAC TGCCATGCAGGGTTCTTCTTGAGAGAAAGTGAAGTGGCTC 635
QY      181 SerCysSerAsnCylBlysSerLeuGluCysThrLysLeuCysLeu---ProGlnIle 199
        |||||
Ddb     636 CCTTCAGGCACCTGCAAGAAAAATGAGGAGTGTATGAAGTTGTGCGCTACCTCCTCGCGTT 695
QY      200 GluAsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhe 219
        |||||
Ddb     696 GCAAATGTCAACAAACCCCGAGACTCAGGTACTGCGGTGCTGTGTGCCCTGGTATTATCTG 755
QY      220 PheGlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMettyrArgtyrGlnArqTrr 239

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Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 6.23e-136 | Length: | 2440 |
| Score: | 1517.00 | Matches: | 302 |
| Percent Similarity: | 70.83% | Conservative: | 38 |
| Best Local Similarity: | 62.92% | Mismatches: | 104 |
| Query Match: | 61.00% | Indels: | 36 |
| DB: | 4 | Gaps: | 7 |

US-09-899-422A-2 (1-455) x US-09-513-007-1 (1-2440)

| | | | |
|----|------|--|------|
| Qy | 1 | MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGluLeuVal | 20 |
| Db | 294 | ATGGGCTCCCAACCGTGCCTGGCCGTGCTGCCACTGGTGTCTCAGCTCTGTTGGCA | 353 |
| Qy | 21 | GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg | 40 |
| Db | 354 | GATGTGTACCCCGCAGGGGTTCAGGGGCTGTGTCCTCACCCCGGGGACCTCGGAGAAGAGA | 413 |
| Qy | 41 | AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr | 60 |
| Db | 414 | GAGAGTCCCTGTCCCAAGGAAATATAACCAACCCGCAAAATAGCACCATTTGCTCCACC | 473 |
| Qy | 61 | LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp | 80 |
| Db | 474 | AAGTGCACAAAGGTACTATCTGTCAATGACTGTCCGGTCCAGGGGAGACACGGAC | 533 |
| Qy | 81 | CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu | 100 |
| Db | 534 | TGCAGGGTGTGCCCTTGGACCTACACTGCCTTGGAGAACCATCTCAGACGATGCCGTG | 593 |
| Qy | 101 | SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp | 120 |
| Db | 594 | AGCTGTCTCCAGGTGCGGGACGAAATGTTCCAGGTGGAGATTTCCGCTTGTGTAGTGGAC | 653 |
| Qy | 121 | ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu | 140 |
| Db | 654 | CGGGACACTGTGTGCGGCTCGAGAGAAACACAGTACCGGGAATFACITGGGTGAACATGCG | 713 |
| Qy | 141 | PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu | 160 |
| Db | 714 | TTCGGTGTCTGAATGACGACCTCTGTCCTCCAAATGGCACAGTGAATATCCCTGCCAGGAG | 773 |
| Qy | 161 | LysGlnAsnThrValCysThrCysHisAlaGlyPheLeuArgGluAsnGlnCysVal | 180 |
| Db | 774 | AGACAGACACCATCTGCCACTGCCATATGGGCTTCTTTCTTAAAGGGCCAAAGTGCATC | 833 |
| Qy | 181 | SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu | 200 |
| Db | 834 | TCCTGTGCATAGTGTGAAGAACAAG--GAGTGGGAGAAAGTATGTCCAAACCCGACCTCA | 890 |
| Qy | 201 | AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe | 220 |
| Db | 891 | ACTGGTAAACACTCTAGGACCCAGGCATCTACAGTACTATTACCCCTGGTGATGTCTTC | 950 |
| Qy | 221 | GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys | 240 |
| Db | 951 | GGGCTTTCCTGGCATCTTCCTCGCTCTGCTCTTAGCATGTCGCTACCAAGCGGTGGAAG | 1010 |
| Qy | 241 | SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGlnGlyGluLeuGlu | 260 |
| Db | 1011 | CCCAAGCTCTACTCCATCTTTCGGGCGACTCCGACTCTGGTAAAGAGGGGGAGCCAGAA | 1070 |
| Qy | 261 | GlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr | 280 |
| Db | 1071 | -----CTCCGTGGTCCCGGCCCGCCAGGCTTCAACCC-----ACC | 1103 |
| Qy | 281 | ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerThrThrThr | 300 |
| Db | 1104 | ACCACCATCTGCTTCAGCTCCACCCCAAGTTCAGACTCTGCTCTCCATTCCTCCCTTACATC | 1163 |
| Qy | 301 | ProGlyAspCysProAsnPhe-----AlaAlaProArgArgGluValAlaProPro | 317 |
| Db | 1164 | TCCTGTGACGGGTCCCAACTCTCGGAGCGGTGCATCTCCCTCCAGCAGACGGCCCGCCC | 1223 |

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318 TyrGlnGlyAlaAspProPheLeu----- 325
   ::  |||  ||||| |||
1224 CATCTAAAGGCTGGCGCCATCTCCCGGGGGCCTCCCGGCCTCCACCCACCTCTGTACCCCG 1283
   ::  |||  ||||| |||
326 -----AlaThrAlaLeu----- 335
   ::||| ||| |||||
1284 GGGCTCCGCGCTCCACCACTCTGTACCCCGGGGCTCCGGCGCTCCACCCACCTCTGTC 1343
   ::||| ||| |||||
336 AsnProLeuGlnLysTrpGluAspSerAla---HisLysProGlnSerLeuAspThrAsp 354
   ::||| ||||| ||||| |||
1344 ACCCATGTTGAGAGTGGGAAGCAGCGCCCCCAGCGCCCTCAGCTCAGCTCGCGGATGCC 1403
   ::||| ||||| |||||
355 AspProAlaThrLeuTyrrAlaValValGluAsnValProProLeuArgTrpLysGluPhe 374
   ::||| ||||| |||||
1404 GACCCCGCGACCTGTACGCGGTGGTGGAGCGGCTGCCCGCTCGGCTGGAGAACGGAGTTG 1463
   ::||| ||||| |||||
375 ValArgArgLeuGlyLeuSerAspHisGluIleCAspArgLeuGluLeuGlnAsnGlyArg 394
   ::||| ||||| |||||
1464 GTGGCGCGCTGGGACTGACGAGCAGCATGCGCGCTGGAGCTGGAGAACGGAGTTG 1523
   ::||| ||||| |||||
395 CysLeuArgGluAlaGlnTyrrSerMetLeuAlaThrTrpArgArgArgThrProArgArg 414
   ::||| ||||| |||||
1524 CACCTGCGCGAGCGCAGTACAGCATCTGCGCGCTGGCGCGCGCACCGCGCGCGCGC 1583
   ::||| ||||| |||||
415 GluAlaThrLeuGluLeuLeuGlyArgValLeuArgAspMetAspLeuGlyCysLeu 434
   ::||| ||||| |||||
1584 GAGGCCACGTGTGAGCTGTGCGCGCGCTCTCAGGACATGAGACCTGCTGGGTGGCTG 1643
   ::||| ||||| |||||
435 GluAspIleGluAlaLeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeu 454
   ::||| ||||| |||||
1644 GAAACATACAGGAGCGCTGGGTGGCGCGCGCGCTCGCGTCCGAGCCCGCCCTCTC 1703

RESULT 11
US-08-286-740-2
: Sequence 2, Application US/08286740
: Patent No. 5561053
: GENERAL INFORMATION:
: APPLICANT: Crowley, Craig W.
: TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
: TITLE OF INVENTION: HOST CELLS
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/286,740
: FILING DATE: 05-AUG-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER:
: REFERENCE/DOCKET NUMBER: 798
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6889 bases
: TYPE: nucleic acid

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STRANDEDNESS: double
TOPOLOGY: linear
US-08-286-740-2

Alignment Scores:

Pred. No.: 5,27e-107 Length: 6889
Score: 1223.50 Matches: 257
Percent Similarity: 64.04% Conservative: 19
Best Local Similarity: 59.63% Mismatches: 61
Query Match: 49.20% Indels: 95
DB: 1 Gaps: 11

US-09-899-422a-2 (1-455) x US-08-286-740-2 (1-6889)

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Db 1665 GGAATATACCCCTCAGGGGTTATTGGACTGGCTCCCTCACCCTAGGGGACAGGAGAGA 1724
Qy 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
Db 1725 GATAGTGTGTGTCCTCCCAAGGAATATATCCACCCTCAAAATAATTGATTGCTGTACC 1784
Qy 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
Db 1785 AAGTGCACAAAGCAACTACTTGTACAAATGACTGTCCAGGCCGGGAGGATACGGAC 1844
Qy 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
Db 1845 TGCAGGAGTGTGACAGCGCTCTTCCCGCTTCAGAAACACCACTCAGACACTGGCTC 1904
Qy 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
Db 1905 AGCTGCTCCAAATGCCAAGGAATATGGTCAAGTGGAGATCTCTTTGCCACAGTGGAC 1964
Qy 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
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Qy 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
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Db 2085 AAACAGAACACCGTGCACCTGCCATGCAGTTCTTCTTAAGAGAAACAGAGTGTGC 2144
Qy 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
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Qy 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhephe 220
Db 2205 AATGTTAAGGCACTGAGGACTCAGGCACCA----- 2237
Qy 221 GlyLeuCysLeuLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTyrLys 240
Db 2237 ----- 2237
Qy 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGlyLysGluGlyLeu---- 259
Db 2238 -----GACAAGAGAGTTGAGCTCAAA 2258
Qy 260 -----GluGlyThrThrThrLysProLeuAlaProAsnProSerPheSerPro 275
Db 2259 ACCCCACTGGTGACACACTACATGCGCGTCCCGAGAGCCCAAACTCTGTGAC 2318
Qy 276 ThrProGlyPheThrProThrLeuGlyPheSerProValProSerSerThrPheThrSer 295
Db 2319 ACACCT-----CCCCGGTCCCGAGGTCGCCAGAGCCC----- 2351

```

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Qy 296 SerSerThrTyrThrProGlyAspCysProAsnPheAlaAlaProArgArg---GluVal 314
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Qy 334 eProAsnProLeuGlnLysTyrGluAsp-----SerAlaHisLysProGlnSer----- 350
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Qy 351 -----LeuAspThrAspAspProAlaThrLeuTyrAlaValValGluAsnVal----- 366
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Qy 367 -----ProProLeuArgTyrLysGluPheValArgLeuGlyLeuSerAspHisG1 384
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Qy 384 uileAspArgLeuGlnLeuGlnAsnGlyArgCysLeu---ArgGluAlaGlnTyrSerMe 403
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RESULT 12

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PCT-US95-09576-2
: Sequence 2, Application PC/TUS9509576
: GENERAL INFORMATION:
: APPLICANT: GENENTECH, INC.
: TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
: TITLE OF INVENTION: HOST CELLS
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/09576
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/286740
: FILING DATE: 05-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: 00,000
: REFERENCE/DOCKET NUMBER: 798PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6889 bases
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
PCT-US95-09576-2

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Alignment Scores:

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| Db | 1605 | ATGGGCCTCCTCCACCGTGTGACTGCTGCTGCCGTGCTGCTGAGCTGTGGTG | 1664 |
| QY | 21 | GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysAsq | 40 |
| Db | 1665 | GGAAATATACCCTCAGGGTTATTGGACTTGGTCCTCACCTAGGGACAGGGAGAAGAGA | 1724 |
| QY | 41 | AspSerValCysProGlnGlyLysTyriIleHisProGlnAsnAsnSerIlecysCysThr | 60 |
| Db | 1725 | GATAGTGTGTGCCCAAGGAAAATAATCCACCCTCAAAATAATTCGATTGCTGTACC | 1784 |
| QY | 61 | LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp | 80 |
| Db | 1785 | AACTGGCCACAAGGAACACTACTTGTACAATGACTTCCAGGCCCGGGCAGGATACGGAC | 1844 |
| QY | 81 | CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu | 100 |
| Db | 1845 | TGCAGGAGTGTGAGACGGCTCTTCACCGCTTCAGAAACCAACCTTCAGACACTGCCTC | 1904 |
| QY | 101 | SerCysSerIlyscysArgLysGluMetGlyGlnValGluIleSerCysThrValasp | 120 |
| Db | 1905 | AGCTGCTCCAATGCGAAGAAATGGGTGAGTGAGATCTCTCTTGACACATGGAC | 1964 |
| QY | 121 | ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu | 140 |
| Db | 1965 | CGGGACACCGTGTGTGGCTGCAGAGAAGAACAGTACCGGCATTTATTGGAGTAAAAACCTT | 2024 |
| QY | 141 | PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu | 160 |
| Db | 2025 | TTCCAGTGCTTCAATGTCAGCCCTCGCCTCAATGGGACCGGTGCACCTCTCTCTGCCAGGAG | 2084 |
| QY | 161 | LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal | 180 |
| Db | 2085 | AAACAGAACACCCGTGTGCACCTGCCATGCAGGTTTTCTTTTAAGAGAAAAACGAGTGTGC | 2144 |
| QY | 181 | SerCysSerAsnCysLysLysSerLeuGluCysThrIlysLeuCysLeuProGlnIleGlu | 200 |
| Db | 2145 | TCCTGTAGTAACTGTAAAGAAACCGTGGAGTCAGCAAGTGTGTGCCTACCCCAGATTGAG | 2204 |
| QY | 201 | AsnValLysGlyThrGluAspSerGlyThrValLeuLeuLeuProLeuValIlePhePhe | 220 |
| Db | 2205 | AATGTTAAGGGCACTGAGGACTCAGGCACCCACA----- | 2237 |
| QY | 221 | GlyLeuCysLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys | 240 |
| Db | 2237 | ----- | 2237 |
| QY | 241 | SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyLeu--- | 259 |
| Db | 2238 | -----GACAAGAGAGTGTGAGCTCAAA | 2258 |
| QY | 260 | -----GluGlyThrThrLysProLeuAlaProAsnProSerPheSerPro | 275 |
| Db | 2259 | ACCCCACTGGTGACACACTCACATGCCCGGTGCCAGAGCCCCCAAATCTGTGAC | 2318 |
| QY | 276 | ThrProGlyPheThrProThrLeuGlyPheSerProValProSerSerThrPheThrSer | 295 |
| Db | 2319 | ACACCT-----CCCCCGTCCACGGTGCACAGGCC----- | 2351 |
| QY | 296 | SerSerThrTyrThrProGlyAspCysProAsnPheAlaAlaProArgArg---GluVal | 314 |
| Db | 2352 | AAATCTGTGACACACTCCCCCATGCCACGGTGCACAGGCCAAAATCTGTGACACA | 2411 |

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2003, 00:13:39 ; Search time 2999 Seconds
(without alignments)
4415.397 Million cell updates/sec

Title: US-09-899-422A-2

Perfect score: 2487

Sequence: 1 MGLSTVPDLLPLVLELLV.....DIEEALCGPALPPAPSLLR 455

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pcp -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
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37: em.htg_vrt:*
38: em.sy:*
39: em.htgo_hum:*
40: em.htgo_mus:*
41: em.htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 2487 | 100.0 | 1368 | 6 | A29098 |
| 2 | 2487 | 100.0 | 2062 | 6 | A21522 |
| 3 | 2487 | 100.0 | 2087 | 9 | HUMTNFR |
| 4 | 2487 | 100.0 | 2111 | 6 | A26412 |
| 5 | 2487 | 100.0 | 2111 | 6 | AX409713 |
| 6 | 2487 | 100.0 | 2111 | 9 | HUMTNFRB |
| 7 | 2487 | 100.0 | 2112 | 9 | HUMTNFRC |
| 8 | 2487 | 100.0 | 2161 | 6 | AR096330 |
| 9 | 2487 | 100.0 | 2161 | 9 | HSTNFR1A |
| 10 | 2487 | 100.0 | 2175 | 6 | A43873 |
| 11 | 2487 | 100.0 | 2175 | 6 | A78738 |
| 12 | 2487 | 100.0 | 2175 | 6 | AR041076 |
| 13 | 2487 | 100.0 | 2175 | 6 | 164751 |
| 14 | 2487 | 100.0 | 2176 | 6 | A19907 |
| 15 | 2487 | 100.0 | 2194 | 9 | BC010140 |
| 16 | 2487 | 99.8 | 2062 | 6 | I43805 |
| 17 | 2471 | 99.4 | 2109 | 9 | AK056611 |
| 18 | 2460 | 98.9 | 2061 | 6 | A20255 |
| 19 | 2444 | 98.3 | 2050 | 9 | HUMTNFRP |
| 20 | 2053.5 | 82.6 | 1331 | 6 | A29103 |
| 21 | 1801.5 | 72.4 | 2171 | 4 | AB051103 |
| 22 | 1738 | 69.9 | 2004 | 4 | SSU19994 |
| 23 | 1670 | 67.1 | 17350 | 9 | AY131997 |
| 24 | 1670 | 67.1 | 188488 | 9 | AC006057 |
| 25 | 1563.5 | 62.9 | 2115 | 10 | AF329976 |
| 26 | 1563.5 | 62.9 | 2130 | 6 | AX401925 |
| 27 | 1563.5 | 62.9 | 2130 | 10 | RATNFR |
| 28 | 1560.5 | 62.7 | 2115 | 10 | AF329977 |
| 29 | 1559.5 | 62.7 | 2115 | 10 | AF329978 |
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| 31 | 1559.5 | 62.7 | 2115 | 10 | AF329980 |
| 32 | 1559.5 | 62.7 | 2115 | 10 | AF329981 |
| 33 | 1521 | 61.2 | 1956 | 10 | MUSTNFR2 |
| 34 | 1521 | 61.2 | 2048 | 10 | MUSTNFR1 |
| 35 | 1521 | 61.2 | 2063 | 10 | MMP55R |
| 36 | 1521 | 61.2 | 2086 | 10 | BC004599 |
| 37 | 1521 | 61.2 | 2154 | 10 | MUSTNFX |
| 38 | 1521 | 61.2 | 2179 | 10 | MMTNFR5 |
| 39 | 1517 | 61.0 | 2440 | 4 | BTU90937 |
| 40 | 1223.5 | 49.2 | 6889 | 6 | I26928 |
| 41 | 1213.5 | 48.8 | 2254 | 9 | HUMTNFR103 |
| 42 | 1192 | 47.9 | 6896 | 6 | AR031375 |
| 43 | 1192 | 47.9 | 6896 | 6 | BD009743 |
| 44 | 1130 | 45.4 | 600 | 6 | A20257 |
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ALIGNMENTS

RESULT 1

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BASE COUNT 429 a 617 c 573 g 443 t

ALIGNMENT SCORES:

Pred. No.: 2,81e-154 Length: 2062
 Score: 2487.00 Matches: 455
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-899-422A-2 (1-455) x A21522 (1-2062)

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 QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
 DB 215 GGAATATACCCCTCAGGGGTATTGGACTGGTCCCTCACCTAGGACAGAGGAGAGA 274
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 QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluLeuSerSerCysThrValAsp 120
 DB 455 AGCTGCTCCAAATGCGCAAGGAAATGGGTGAGGTGAGATCTCTTCTTCACAGTGGAC 514
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 QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGlnLysGlnGlyGluLeuGlu 260
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 DB 1295 AGCAGCACAGATCGATCGCTGGAGCTGCAGAACGGCGCTGCTCGCGAGGCGCAA 1354
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 DB 1355 TACAGCATGTGCGGACCTGGAGCGCGCAGCGCGCGCGGCGGAGCGCAGCTGGAGCTG 1414
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 QY 441 LeuCysGlyProAlaLeuProProAlaProSerLeuLeuArg 455
 DB 1475 CTTTGGGCGCCCGCGCTCCCGCGCGCGCGCGCGCTTCTCAGA 1519

RESULT 3

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 DEFINITION Human tumor necrosis factor receptor mRNA, complete cds.
 ACCESSION M33294
 VERSION M33294.1 GI:339744
 KEYWORDS cell surface receptor; tumor necrosis factor receptor.
 SOURCE Human placenta, CDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2087)
 AUTHORS Schall,T.J., Lewis,M., Koller,K.J., Lee,A.L., Rice,G.C., Wong,G.H.,
 Gatanaga,T., Granger,G.A., Lentz,R., Raab,H., Kohn,W.J. and
 Goeddel,D.V.
 TITLE Molecular cloning and expression of a receptor for human tumor
 necrosis factor
 JOURNAL Cell 61 (2), 361-370 (1990)
 MEDLINE 90235285
 PUBMED 2158863
 COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
 by T.Schall, 26-MAR-1990.
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 /db_xref="GI:339745"
 /translation="MGLSTVPDLLLPLVLELLVLPSCVIGLVPHLGDREKRDVSC"


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QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
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QY 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
Db 307 GATAGTGTGTGTCACAGGAATAATATCCACCCTCAAAATAATTCGATTTCGTGTACC 366
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QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
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QY 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
Db 967 GGAACCTACTAAGCCCTCGCCCAACCCCAAGCTTCAGTCCACCTCCAGGCTTCACC 1026
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QY 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
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RESULT 6

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HUMTNFRB
LOCUS HUMTNFRB 2111 bp mRNA linear PRI 03-AUG-1993
DEFINITION Homo sapiens tumor necrosis factor receptor mRNA, complete cds.
ACCESSION M58286.1
VERSION M58286.1 GI:339753
KEYWORDS tumor necrosis factor receptor.
SOURCE Human cell line HL60, CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 2111)
AUTHORS Loetscher,H., Pan,Y.C., Lahm,H.W., Gentz,R., Brockhaus,M.,
Tabuchi,H. and Lesslauer,W.
TITLE Molecular cloning and expression of the human 55 kd tumor necrosis
factor receptor
JOURNAL Cell 61 (2), 351-359 (1990)
MEDLINE 90235284
PUBMED 2158862
FEATURES
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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| Db | 1267 | GCCTGTGTGAGAACGTGCCCCGTTTCGCTGGAAGCAATTCGTGCGCGCCTAGGCGTG | 1326 |
| Qy | 381 | SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln | 400 |
| Db | 1327 | AGCGACCACAGATCGATCGCTGGAGCTCGAGAACGGCGCTCCCTGCGCGAGGCGCAA | 1386 |
| Qy | 401 | TyrSerMetLeuAlaThrTrpArgArgGlnThrProArgGluAlaThrLeuGluLeu | 420 |
| Db | 1387 | TACAGCATGTGGCGACCTGGAGCGCGCACGCCGCGCGGCGAGGCCACGCTGGAGCTG | 1446 |
| Qy | 421 | LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAla | 440 |
| Db | 1447 | CTGGAGCGCGTGTCCCGCATGAGACCTGCTGGCTCGCTGGAGGACATCGAGGAGCG | 1506 |
| Qy | 441 | LeuCysGlyProAlaLeuLeuProProAlaProSerLeuLeuArg | 455 |
| Db | 1507 | CTTTGCGCGCGCGCGCTCCCGCGCGCGCGCCAGTCTTCTCAGA | 1551 |
| RESULT 7 | | | |
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| LOCUS | | | |
| DEFINITION | HUMTNFRC | 2112 bp mRNA linear PRI 03-AUG-1993 | |
| ACCESSION | M63121 | M75861 | |
| VERSION | M63121.1 | GI:339755 | |
| KEYWORDS | tumor necrosis factor receptor. | | |
| SOURCE | Human cDNA to mRNA. | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| AUTHORS | Hämmler, A., Maurer-Fogy, I., Kronke, M., Scheurich, P., Pfizenmayer, K., Lantzi, M., Olsson, I., Hauptmann, R., Stratowa, C. and Adolf, G.R. | | |
| TITLE | Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein | | |
| JOURNAL | DNA Cell Biol. 9 (10), 705-715 (1990) | | |
| MEDLINE | 91090841 | | |
| PUBMED | 1702293 | | |
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Alignment Scores:

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Pred. No.: 2,89e-154 Length: 2112
Score: 2487.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-899-422A-2 (1-455) * HUMTNPFC (1-2112)

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QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluysArg 40
Db 267 GGAATATACCCCTCAGGGGTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAGAGA 326
QY 41 AspSerValCysProGlnClyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
Db 327 GATAGTGTGTGTCCTCCCAAGGAATAATATCCACCTCAAAATAATTCGATTTCGTGTACC 386
QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlnAspThrAsp 80
Db 387 AAGTCCCAAGGAACCTACTTGTACATGACTGTCAGGGCCGCGGGCAGCATACGGAC 446
QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
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QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
Db 507 ACCTGCTCCAAATGCGGAAGAAATGGTCAAGTGGAGATCTCTTTCACATGGAC 566
QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
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QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
Db 687 AAACAGACACCGTGTGCACCTGCCATCGAGTTCTTCTTAAGAGAAACACGATGCTC 746
QY 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
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Db 927 TCCAAGCTCTACTCCATTGTTGTGGAAATCGACACCTGAAAGAGGGGGAGCTTCAA 986
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Db 987 GGAATCTACTAGACCCCTGGCCCCCAACCAACAGCTTCAGTCCCACTCCAGGCTTACC 1046
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Db 1047 CCCACCTGGGCTTCAGTCCCGTCCCGAGTTCACCTTCACCTCCAGCTCCACCTATACC 1106
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LOCUS AR096330 2161 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 1 from patent US 6007995.
ACCESSION AR096330
VERSION AR096330.1 GI:10025045
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2161)
AUTHORS Baker,B.F. and Cowser,L.M.
TITLE Antisense inhibition of TNFR1 expression
JOURNAL Patent: US 6007995-A 1 28-DEC-1999;
FEATURES
source
location/Qualifiers
BASE COUNT 459 a 642 c 604 g 456 t
ORIGIN
Alignment Scores: 2,97e-154 Length: 2161
Score: 2487.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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DB: 6 Gaps: 0

US-09-899-422A-2 (1-455) * AR096330 (1-2161)

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DB 1396 AGCGACCAAGATGCTGCCTGGAGCTGCAGAACGGCGCCTGCCGTGCGGAGGCGCAA 1455
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RESULT 10
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 DEFINITION Sequence 1 from Patent EP0657536.
 ACCESSION A43873
 VERSION A43873.1 GI:2299022
 KEYWORDS unidentified.
 SOURCE unidentified.
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 2175)
 AUTHORS Wallach,D., Brackebusch,C., Varfolomeev,E. and Batkin,M.
 TITLE Proteases capable of shedding the soluble TNF-receptor and TNF-R derived peptides and antibodies against the proteases inhibiting the shedding
 JOURNAL Patent: EP 0657536-A 1 14-JUN-1995;
 YEDA RES & DEV (IL)
 COMMENT Other publication ZA 9407962 951121
 Other publication JP 7194376 950801
 Other publication AU 7574294 950504
 Other publication CA 2133872 950413.

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BASE COUNT 474 a 641 c 604 g 456 t
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 Pred. No.: 2,99e-154 Length: 2175
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 Query Match: 100.00% Indels: 0
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US-09-899-422A-2 (1-455) x A43873 (1-2175)

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LOCUS AR041076 2175 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5811261.
ACCESSION AR041076
VERSION AR041076.1 GI:5961572
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
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Unclassified.
1 (bases 1 to 2175)
Wallach,D., Nophar,Y., Kemper,O., Engelmann,H., Brakebusch,C. and
Aderka,D.
Expression of the recombinant tumor necrosis factor binding protein
I (TBP-I)
Patent: US 5811261-A 1 22-SEP-1998;
Location/Qualifiers
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BASE COUNT 474 a 541 c 504 g 456 t
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Alignment Scores:
Score: 2,99e-154 Length: 2175
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Unclassified.

1 (bases 1 to 2175)
Wallach,D., Nophar,Y., Kemper,O., Engelmann,H., Brakebusch,C. and
Aderka,D.

Expression of the recombinant tumor necrosis factor binding protein
I (TBP-I)

Patent: US 5811261-A 1 22-SEP-1998;
Location/Qualifiers

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/organism="unknown"

BASE COUNT 474 a 541 c 504 g 456 t
ORIGIN

Alignment Scores:

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Pred. No.: 2487.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-899-422A-2 (1-455) x AR041076 (1-2175)

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| QY | 21 | GlyIleotyProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg | 40 |
| DB | 316 | GGAAATATACCCCTCAGGGGTTATTTGGACTGGTCCCTCACCTAGGGACACGGGAGAGAGA | 375 |
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| DB | 796 | TCCTGTAGTAACCTGAAGAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCAGATTGAG | 855 |
| QY | 201 | AsnValLysGlyThrGluAspSerGlyThrValLeuLeuProLeuValIlePhePhe | 220 |
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| DB | 916 | GGTCTTTGCCCTTTATCCCTCCCTTCATTTGGTTTAATGTATCGCTACCAACGGTGAAG | 975 |
| QY | 241 | SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu | 260 |
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401 TyrSerMetLeuAlaThrTrpArgArgThrProArgArgGluAlaThrLeuGluLeu 420
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LOCUS A19907 2176 bp DNA linear PAT 04-OCT-1994
DEFINITION Synthetic nucleotide sequence Type I TNF receptor gene.
ACCESSION A19907
VERSION A19907.1 GI:641222
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 2176)
AUTHORS Wallach,D., Nophar,Y., Kemper,O., Engelmann,H., Brakebusch,C. and Aderka,D.
TITLE Expression of the recombinant tumor necrosis factor binding protein I (TBP-I)
JOURNAL Patent: EP 0433900-A 28 JUN-1991;
YEDA RESEARCH AND DEVELOPMENT COMPANY LIMITED
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Query Match: 100.00% Indels: 0
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US-09-899-422A-2 (1-455) x A19907 (1-2176)

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QY 41 AspSerValCysProGlnGlyIleGlyTyrIleHisProGlnAsnAsnSerIleCysThr 60
DB 376 GATAGTGTGTGCCCAAGSAAATATATCCACCCTCAAAATAATTGCTGTGTACC 435
QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyInAspThrAsp 80
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DB 1456 TACAGCATGCTGGGACCTGGAGGCGGCGCACCGCGCGGCGGAGGCCACGCTGAGCTG 1515
QY 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
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QY      401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420
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Search completed: June 9, 2003, 02:13:37
Job time : 3023 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 8, 2003, 20:48:38 ; Search time 1864 seconds
(without alignments)
11885.958 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 4 | 703.6 | 51.4 | 741 | 13 | BT860918 |
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| 11 | 668.6 | 48.9 | 974 | 12 | BT180101 |
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| 13 | 667 | 48.8 | 718 | 12 | BG680679 |
| 14 | 647.2 | 47.3 | 994 | 14 | BM800044 |
| 15 | 638.4 | 46.7 | 837 | 9 | AL522989 |
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| 18 | 625 | 45.7 | 636 | 12 | BG035257 |
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VERSION
BM923204.1 GI:19373583
KEYWORDS
EST.
SOURCE
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ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1076)
AUTHORS
NIH-MGC.http://mgc.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cygabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12803 row: b column: 06
High quality sequence stop: 727.
Location/Qualifiers
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oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
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023. Note: this is a NIH MGC Library."
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QY 1033 GCCCAAGCCACAGAGCCTAGACACTGATGATGATGATGATGATGATGATGATGATGATGAT 1092
DB 494 GCCCAAGCCACAGAGCCTAGACACTGATGATGATGATGATGATGATGATGATGATGATGAT 553
QY 1093 AACGTGCCCCGTTGCGCTGGAAGAAATTCGTGGCGGCCCTAGGGCTGAGGCCACACAG 1152
DB 554 AACGTGCCCCGTTGCGCTGGAAGAAATTCGTGGCGGCCCTAGGGCTGAGGCCACACAG 613
QY 1153 ATCGATCGCTGGAGCTGCAGAGGGGCTGCTGCGGAGGGCGCAATACAGATGCTG 1212
DB 614 ATCGATCGCTGGAGCTGCAGAGGGGCTGCTGCGGAGGGCGCAATACAGATGCTG 673
QY 1213 CGGACCTGGAGGGCGGCCACGCCGGCGGCGAGCGCCAGCTGAGCTGCTGGGACGCGTG 1272
DB 674 CGGACCTGGAGGGCGGCCACGCCGGCGGCGAGCGCCAGCTGAGCTGCTGGGACGCGTG 733
QY 1273 CTCGCGACATGGACCTGCTGGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1332
DB 1332 CTCGCGACATGGACCTGCTGGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG

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734 CTCGCGACATGGACCTGCTGGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 793

1333 GCGGCGCTCCCG 1368

794 GNCGCCCTCCCG 829

RESULT 2

B0723672

LOCUS

DEFINITION

AGENCY: 849850 Lupski_dorsal_root_ganglion Homo sapiens CDNA

clone IMAGE:6184295 5', mRNA sequence.

ACCESSION

B0723672

VERSION

B0723672.1 GI:21862569

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 931)

AUTHORS

NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CNA Library Preparation: Life Technologies, Inc.

CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM13573 row: d column: 24

High quality sequence stop: 607.

Location/Qualifiers

1..931

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6184295"

/clone.lib="Lupski_dorsal_root_ganglion"

/sex="male"

/tissue_type="dorsal root ganglia"

/dev_stage="adult, 36 yr"

/lab_host="DH10B"

/Note="Vector: PCMV-SPORT6 (Life Technologies); Site_1:

NotI; Site_2: SalI; cDNA made by oligo-dT priming.

Directionally cloned using the following adaptors:

5'-TCGACCCACGCGTCCG-3' and

5'-GACTAGTTCTAGATCGCGGCGCGCGCT(15)-3'. Size selected >

1 kb for average insert length 1.7 kb. This is a primary

library, non-amplified. Library constructed by Life

Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor

College of Medicine) and is available through Life

Technologies."

BASE COUNT 218 a 283 c 224 g 204 t 2 others

ORIGIN

Query Match

Best Local Similarity 58.7%; Score 803.6; DB 14; Length 931;

Matches 862; Conservative 0; Mismatches 40; Indels 5; Gaps 3;

QY 111 GGAGAAGAGATAGT 170

DB 1 GGAGAAGAGATAGT 60

QY 171 TTGCTGTACCAAGTGCACAAAGAACCTACTTGTACAAATGACTGTCCAGCCCGGGGCA 230

DB 61 TTGCTGTACCAAGTGCACAAAGAACCTACTTGTACAAATGACTGTCCAGCCCGGGGCA 120

QY 231 GGATACGGACATGAGGGAGTGTGAGAGCGGCTTCCACCTTCAGAAAACACCTCAG 290

DB 121 GGATACGGACATGAGGGAGTGTGAGAGCGGCTTCCACCTTCAGAAAACACCTCAG 180

[illegible]

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QY 721 TCAAGCTCTACTCATTTGTTGGGAAATCGACACCTGAAAAA 765
|||||
Db 913 TCCAAGCTCTACTCATTTGTTGGGAAATCGACACCTGAAAAA 957
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RESULT 4
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DEFINITION 741 bp mRNA linear EST 10-OCT-2001
603390284F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5399108 5',
mRNA sequence.
ACCESSION BI860918
VERSION BI860918.1 GI:16001653
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 741)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-re@mail.nih.gov
Tissue Procurement: DCTD/OMP
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12017 row: h column: 21
High quality sequence stop: 740.
Location/Qualifiers
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/clone="IMAGE:5399108"
/tissue_lib="NIH_MGC_87"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/site="Organ: breast; Vector: pCMV-Sport6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 167 a 229 c 175 g 170 t
ORIGIN

Query Match 51.4%; Score 703.6; DB 13; Length 741;
Best Local Similarity 98.5%; Pred. No. 3.5e-163;
Matches 731; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

QY 257 GGGGCTCTTACCGCTTCAGAAAACACCTCAGACACTGCTCAGCTGCTCCAAATGCC 316
|||||
Db 1 GGGGCTCTTACCGCTTCAGAAAACACCTCAGACACTGCTCAGCTGCTCCAAATGCC 60
|||||

QY 317 GAAAGAAATGGTTCAGGTGGAGATCTCTTTCACACAGTGGACCGGACACCGGTGTG 376
|||||
Db 61 GAAAGAAATGGTTCAGGTGGAGATCTCTTTCACACAGTGGACCGGACACCGGTGTG 120
|||||

QY 377 GCTGAGGAGAACAGTACCGGCATTATTGGAGTGAACCTTTTCCAGTCTCAATT 436
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Db 121 GCTGAGGAGAACAGTACCGGCATTATTGGAGTGAACCTTTTCCAGTCTCAATT 180
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QY 437 GCAGCTCTGCTCAATGGGACCGTGCACCTCTCTCTCCAGGAGAAACAGAACCGGT 496
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Db 181 GCAGCTCTGCTCAATGGGACCGTGCACCTCTCTCTCCAGGAGAAACAGAACCGGT 240
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QY 497 GCACCTGCACGACAGTTCTTTCTPAGAGAAAACAGAGTGTCTCTCTGTAGTACTGTA 556
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Db 241 GCACCTGCACGACAGTTCTTTCTPAGAGAAAACAGAGTGTCTCTCTGTAGTACTGTA 300
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QY 557 AGAAAAGCCTGGAGTGCACGAAGTTGTGCTTACCCAGATTGAGAAATGTTAAGGCAC 616
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Best Local Similarity 99.4%; Pred. No. 1.5e-159;
Matches 700; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 665 TTGCGCTTTATCCCTCCCTCTTCATGTTTAAATGATCGCTACCAACGGTGGAGTCCA 724
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QY 725 AGCTCTACTCCATTTGTTGTGGAAATGCACACCTGAAAGAGAGGGGAGCTTGAAGAA 784
Db 61 AGCTCTACTCCATTTGTTGTGGAAATGCACACCTGAAAGAGAGGGGAGCTTGAAGAA 120
QY 785 CTACTACTAAGCCCTCGGCCCAAAACCAAGCTTCAGTCCCACTCCAGGCTTCACCCCA 844
Db 121 CTACTACTAAGCCCTCGGCCCAAAACCAAGCTTCAGTCCCACTCCAGGCTTCACCCCA 180
QY 845 CCCTGGGCTTCAGTCCGCTGCCAGTCCACCTTCACCTCCAGCTCCACCTATACCCCG 904
Db 181 CCCTGGGCTTCAGTCCGCTGCCAGTTCACCTTCACCTCCAGCTCCACCTATACCCCG 240
QY 905 GTGACTGTCCCAACTTTGGGCTCCCGCAGAGAGGTGGCACCCTATCAGGGGGCTG 964
Db 241 GTGACTGTCCCAACTTTGGGCTCCCGCAGAGAGGTGGCACCCTATCAGGGGGCTG 300
QY 965 ACCCATCTTTCGGAGAGCCCTCGCTCGGACCCCAATCCCAACCCCTTCAGAGTGGG 1024
Db 301 ACCCATCTTTCGGAGAGCCCTCGCTCGGACCCCAATCCCAACCCCTTCAGAGTGGG 360
QY 1025 AGGACAGCGCCACAAAGCCACAGAGCTAGACACATGATGACCCCGCGAGCTGTACGCG 1084
Db 361 AGGACAGCGCCACAAAGCCACAGAGCTAGACACATGATGACCCCGCGAGCTGTACGCG 420
QY 1085 TGGTGAGAACGTGCCCGCTTTCGCTGGAAGGAATTCGTGCGGCGCCCTAGGGCTGAGCG 1144
Db 421 TGGTGAGAACGTGCCCGCTTTCGCTGGAAGGAATTCGTGCGGCGCCCTAGGGCTGAGCG 480
QY 1145 ACCACAGATCATCGCTGGAGCTGCAGACGGGGCTGCTGCGGAGGCGCAATACA 1204
Db 481 ACCACAGATCATCGCTGGAGCTGCAGACGGGGCTGCTGCGGAGGCGCAATACA 540
QY 1205 GCATGCTGCGACCTTGGAGCGCGCCAGCCCGCGCGAGGCGCAGCTGGAGCTGCTGG 1264
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QY 1265 GACGCGTCTCGCGACATGGACCTGCTGGGCTGCTGGAGGACATCGAGGAGGGCGCTTT 1324
Db 601 GACGCGTCTCGCGACATGGACCTGCTGGGCTGCTGGAGGACATCGAGGAGGGCGCTTT 660
QY 1325 GGGGCGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
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LOCUS AUI31978 NT2RP3 Homo sapiens cDNA clone NT2RP3003570 5', mRNA
DEFINITION sequence.
ACCESSION AUI31978
VERSION AUI31978.1 GI:10992332
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 761)
Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saibo.K., Kawai.Y.,
Yamamoto.J., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and
Isogai.T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
```

```
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 252-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1..761
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cells after 2-weeks retinoic acid (RA) induction"
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Best Local Similarity 99.1%; Pred. No. 6.1e-158;
Matches 694; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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QY 61 GGAATATACCCCTCAGGGGTTATTGGACTGTGCTCCCTCCTAGGGGACAGGAGAGAGA 120
Db 122 GGAATATACCCCTCAGGGGTTATTGGACTGTGCTCCCTCCTAGGGGACAGGAGAGAGA 181
QY 121 GATAGTGTCTGCCCAAGGAAATATATCCACCTCAAAATTAATTCGATTTGCTGTACC 180
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QY 181 AAGTGCCACAAAGGAACTTACTTGTACAATGACTGTCCAGGGCGGGGAGGATACGGAC 240
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QY 241 TGCAGGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAACACCTCAGACACTGCCTC 300
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QY 301 AGCTGCTCAAAATGCCGAAGGAAATGGCTGAGTGGAGATCTCTTCTTCCACAGTGGAC 360
Db 362 AGCTGCTCAAAATGCCGAAGGAAATGGGTGAGTGGAGATCTCTTCTTCCACAGTGGAC 421
QY 361 CGGGACACCGTGTGTGCTGCAGGAAAGACCACTACCGCATTTATTTGGAGTGAACACCTT 420
Db 422 CGGGACACCGTGTGTGCTGCAGGAAAGACCACTACCGCATTTATTTGGAGTGAACACCTT 481
QY 421 TTCCAGTGTTCAAATTCAGACCTCTCCCTCAATGGAGACCTGCACCTCTCTTCCAGGAG 480
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QY 481 AATACAGACACCGTGTGCACCTGCCATGAGGCTTCTTTCTTCTAGAGAAACAGTGTGTC 540
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Db 662 AATGTTAAGGGCACTGAGGACTCAGCCACACCAATGCTTGTGCTCCCTCGNCATTTCTT 721
QY 660 TGGTCTTTTGGCTTTTATCCCTCCTCTTCATTTGTTTAATG 699
Db 722 TGGTCTTTTGGCTTTTATCCCTNCTCTTCATTTGTTTAATG 761
```

Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 252-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES
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/cell_line="NT2"
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cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT 178 a 199 c 201 g 179 t 4 others
ORIGIN

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|------------|--|-----------|----------|-----------|----------|---|
| TITLE | Full-length cDNA libraries and normalization | | | | | |
| JOURNAL | Unpublished (2001) | | | | | |
| COMMENT | Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr. | | | | | |
| FEATURES | Location/Qualifiers | | | | | |
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| | /organism="Homo sapiens" | | | | | |
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| | /tissue_type="placenta" | | | | | |
| | /note="vector: pcwvSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcwvSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : | | | | | |
| | http://fulllength.invitrogen.com" | | | | | |
| BASE COUNT | 231 a | 258 c | 259 g | 221 t | 6 others | |
| ORIGIN | | | | | | |
| | Query Match 49.6%; Score 678.2; DB 9; Length 975; | | | | | |
| | Best Local Similarity 97.9%; Pred. No. 6.9e-157; | | | | | |
| | Matches 704; Conservative 4; Mismatches 8; Indels 3; Gaps 2 | | | | | |
| Qy | 1 | ATGGGCCTC | CACCGTGC | CACTGCTG | CTGCCAC | TGTGTCCTCGAGCTGTTGGTG 60 |
| Db | 256 | ATGGGCCTC | CACCGTGC | CACTGCTG | CTGCCAC | TGTGTCCTCGAGCTGTTGGTG 315 |
| Qy | 61 | GGAATATAC | CCCTCAGG | GGTTATTGG | ACTGGTGC | CTCACCTAGGGACAGGAGAAGA 120 |
| Db | 316 | GGAATATAC | CCCTCAGG | GGTTATTGG | ACTGGTGC | CTCACCTAGGGACAGGAGAAGA 375 |
| Qy | 121 | GATAGTGTG | TCTCCC | AAGAAATA | TATTCAC | CCCTCAAATAATTCGATTTCGTGTACC 180 |
| Db | 376 | GATAGTGTG | TCTCCC | AAGAAATA | TATTCAC | CCCTCAAATAATTCGATTTCGTGTACC 435 |
| Qy | 181 | AAGTGCCAC | AAAGAAC | CTACTTGT | TACAACTG | TCAGGCCCCGGGCAGGATACGGAC 240 |
| Db | 436 | AAGTGCCAC | AAAGAAC | CTACTTGT | TACAACTG | TCAGGCCCCGGGCAGGATACGGAC 495 |
| Qy | 241 | TGCAGGAGT | GTGAGG | GGCTCCTTC | CACCGCTT | CAGAAAACCACTCAGACACTGCCTC 300 |
| Db | 496 | TGCAGGAGT | GTGAGG | GGCTCCTTC | CACCGCTT | CAGAAAACCACTCAGACACTGCCTC 555 |
| Qy | 301 | AGCTGCTCC | AAATCCG | AAAGAAAT | GGGTGAG | TGGAGATCTCTTTTTCACAGCTGGAC 360 |
| Db | 556 | AGCTGCTCC | AAATCCG | AAAGAAAT | GGGTGAG | TGGAGATCTCTTTTTCACAGCTGGAC 615 |
| Qy | 361 | CGGACACCG | TGTGTGG | CTGCAGG | AAGAAC | CAGTACCGGCGAATATTGAGAGTGA AACCTT 420 |
| Db | 616 | CGGACACCG | TGTGTGG | CTGCAGG | AAGAAC | CAGTACCGGCGAATATTGAGAGTGA AACCTT 675 |
| Qy | 421 | TTCCAGTGT | TCAATTG | CAGCCTCTG | CCCTCAAT | GGACCGTGCACCTCTCTCTCCG CAGGAG 480 |
| Db | 676 | TTCCAGTGT | TCAATTG | CAGCCTCTG | CCCTCAAT | GGACCGTGCACCTCTCTCTCCG CAGGAG 735 |
| Qy | 481 | AAACAGAAC | ACCGCTG | TCACCTGC | ATGCAGG | TTCTTTTCTTAAGAGAAACACGAGTGTGC 540 |
| Db | 736 | AAACAGAAC | ACCGCTG | TCACCTGC | ATGCAGG | TTCTTTTCTTAAGAGAAACACGAGTGTGC 795 |
| Qy | 541 | TCCTGTAGT | AACCTGT | AAAGAAAG | CCCTGGAG | TGCAGTGCACGAAGTTG-TGCC TACCCGAGTTGA 599 |
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| Qy | 600 | GAATGTTAA | GGGCACTG | AGGACTC | AGGCAC | CACTGCTGTTGCCCTCGTGTCATTTTCTT 659 |
| Db | 856 | GAATGTTAA | GGGCACTG | AGGACTC | AGGCAC | CACTGCTGTTGCCCTCGTGTCATTTTCTT 915 |

| TITLE | | Full-length cDNA libraries and normalization | |
|-----------------------|--|--|--|
| JOURNAL | | Unpublished (2001) | |
| COMMENT | | Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr. Location/Qualifiers | |
| FEATURES | | 1. 975 | |
| source | | /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CS0D1082YA01" /clone_lib="UFL_NFL006_PL2" /tissue_type="placenta" /note="vector: pcwvSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcwvSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com" | |
| BASE COUNT | 231 a 258 c 259 g 221 t 6 others | | |
| ORIGIN | | | |
| Query Match | 49.6%; Score 678.2; DB 9; Length 975; | | |
| Best Local Similarity | 97.9%; Pred. No. 6.9e-157; | | |
| Matches 704; | Conservative 4; Mismatches 8; Indels 3; Gaps 2 | | |
| Qy | 1 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACGTGGTGCTCTCTCGAGCGTGTGGTG 60 | | |
| Db | | | |
| 256 | ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACGTGGTGCTCTCTCGAGCGTGTGGTG 315 | | |
| Qy | 61 GGAATATACCCCTCAGGGGTATTGGACTGGTGCTCCTCACCTAGGGACAGGAGAGAGA 120 | | |
| Db | | | |
| 316 | GGAATATACCCCTCAGGGGTATTGGACTGGTGCTCCTCACCTAGGGACAGGAGAGAGA 375 | | |
| Qy | 121 GATAGTGTGTCTCCCAAGGAAATATATCACACCTCAAAATAATTTCGATTTCGTGTACC 180 | | |
| Db | | | |
| 376 | GATAGTGTGTCTCCCAAGGAAATATATCACACCTCAAAATAATTTCGATTTCGTGTACC 435 | | |
| Qy | 181 AAGTGCCACAAAGAACCTACTTGTACAAAGACTGTTCAGGCCCGGGCAGAGATACGGAC 240 | | |
| Db | | | |
| 436 | AAGTGCCACAAAGAACCTACTTGTACAAAGACTGTTCAGGCCCGGGCAGAGATACGGAC 495 | | |
| Qy | 241 TGCAGGAGTGTGAGAGCGGCTCTTCCACCGCTTCAGAAAACCACTCAGACACTGCCTC 300 | | |
| Db | | | |
| 496 | TGCAGGAGTGTGAGAGCGGCTCTTCCACCGCTTCAGAAAACCACTCAGACACTGCCTC 555 | | |
| Qy | 301 AGCTGTCTCCAAATCCGAAAGAAATGGGTGAGTGGAGATCTCTTTTGCACAGTGGAC 360 | | |
| Db | | | |
| 556 | AGCTGTCTCCAAATCCGAAAGAAATGGGTGAGTGGAGATCTCTTTTGCACAGTGGAC 615 | | |
| Qy | 361 CGGACACCGTGTGTGGCTGCAGGAAGAACCAAGTACCGGCAATTATGGAGTGAACACCTT 420 | | |
| Db | | | |
| 616 | CGGACACCGTGTGTGGCTGCAGGAAGAACCAAGTACCGGCAATTATGGAGTGAACACCTT 675 | | |
| Qy | 421 TTCCAGTGTTCAAATTGCAGCTCTGCCTCAATGGACCGTGCACCTCTCTCTGCCAGGAG 480 | | |
| Db | | | |
| 676 | TTCCAGTGTTCAAATTGCAGCTCTGCCTCAATGGACCGTGCACCTCTCTCTGCCAGGAG 735 | | |
| Qy | 481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTCTTTTCTAAGAGAAACACGAGTGTGC 540 | | |
| Db | | | |
| 736 | AAACAGAACACCGTGTGCACCTGCCATGCAGTGTTCCTTCTAAGAGAAACACGAGTGTGC 795 | | |
| Qy | 541 TCCTGTAGTAACTGAAGAAAGCCTGGAGTGCAGAAAGTTG-TGCCATACCCGATTGA 599 | | |
| Db | | | |
| 796 | TYCTGTAGTAACTGDAGAAAGCCTGGAGTGCAGAAAGTTGTTGTCCTACCCGATTGA 855 | | |
| Qy | 600 GAATGTTAAGGGCACTGAGGACTCAGGCACCACTGCTGTTGCCCTTGTCATTTTCTT 659 | | |
| Db | | | |
| 856 | GAATGTTAAGGGCACTGAGGACTCAGGCACCACTGCTGTTGCCCTTGTCATTTTCTT 915 | | |

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QY 660 TGGTCTTTGCTTTTATCCCTCTCTCTCATTTGGTTTAAATGATATCGCTACCAACGGTGA 718
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Db 916 TGGTCTTTGCTTTT-ATCCCTCTCTCTCATTTGGTTTAAATGATATCGCTACCAACGGTGA 972

RESULT 10
BM742388
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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mRNA linear EST 01-MAR-2002
mRNA sequence.
BM742388
BM742388.1 GI:19063703
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 669)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 5 row: C column: 12
High quality sequence stop: 669.
Location/Qualifiers
1..669
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-5-C12"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/lab_host="Top10F"
/Note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 50nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
BASE COUNT 128 a 239 c 193 g 109 t
ORIGIN

Query Match 48.9%; Score 669; DB 14; Length 669;
Best Local Similarity 100.0%; Pred. No. 1.2e-154;
Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 688 ATTGGTTTAAATGATATCGCTACCAACGGTGAAGTCCAAAGCTCTACTCCATTGTTGGG 747
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Db 1 ATTGGTTTAAATGATATCGCTACCAACGGTGAAGTCCAAAGCTCTACTCCATTGTTGGG 60
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QY 748 AAATCGACACCTGAAAAAGAGGGGAGGCTTGAAGGAACCTACTACTAAGCCCTGGCCCA 807
|||||

61 AAATCGACACCTGAAAAAGAGGGGAGGCTTGAAGGAACCTACTACTAAGCCCTGGCCCA 120
808 AACCCAAAGCTTCAGTCCACATCCAGGCTTCACCCACCCAGCTTCAGTCCCTGCCC 867
|||||
Db 121 AACCCAAAGCTTCAGTCCACATCCAGGCTTCACCCACCCAGCTTCAGTCCCTGCCC 180
|||||
QY 868 AGTTCCACCTTCACCTCCAGCTTCACCTATATACCCCGGTGACTGTCCCAACTTTCCGGCT 927
|||||
Db 181 AGTTCCACCTTCACCTCCAGCTTCACCTATATACCCCGGTGACTGTCCCAACTTTCCGGCT 240
|||||
QY 928 CCCCGCAGAGAGTGGGACACCTATATCAGGGGGGTGACCCCATCTCTTGGCAGACCCCTC 987
|||||
Db 241 CCCCGCAGAGAGTGGGACACCTATATCAGGGGGGTGACCCCATCTCTTGGCAGACCCCTC 300
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QY 988 GCCTCCGACCCCATCCCAACCCCTTCAGAAAGTGGAGGACAGCCCAAGCCACAG 1047
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QY 1168 CTGAGAAAGCGGCGCTGCTGCGGAGGCGCAATACAGCTGTGGCAGCTGGAGGCGG 1227
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Db 481 CTGAGAAAGCGGCGCTGCTGCGGAGGCGCAATACAGCTGTGGCAGCTGGAGGCGG 540
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QY 1228 CGCAGCGCGCGGCGGACGCTGTGAGCTGTGGACGCGTCTCCGGGACATGAC 1287
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Db 541 CGCAGCGCGCGGCGGACGCTGTGAGCTGTGGACGCGTCTCCGGGACATGAC 600
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QY 1288 CTGCTGGGCTGCTGCGGAGGACATCGAGGAGCGCTTTCGCGCGCGCGCTCCCGCC 1347
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Db 601 CTGCTGGGCTGCTGCGGAGGACATCGAGGAGCGCTTTCGCGCGCGCGCTCCCGCC 660
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QY 1348 GCGGCCAGT 1356
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Db 661 GCGGCCAGT 669

RESULT 11
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LOCUS
DEFINITION 602329676F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4431019 5',
mRNA sequence.
ACCESSION BG180101
VERSION BG180101.1 GI:12698804
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 974)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: DCTD/DP
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10185 row: g column: 20
High quality sequence stop: 657.
Location/Qualifiers
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/organism="Homo sapiens"
source

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UI-H-D10-ato-h-17-0-UI.s1 NCI_CGAP_D10 Homo sapiens cDNA clone
IMAGE:5862208 3', mRNA sequence.
BM989994
BM989994.1 GI:19709383
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NC1 (bases 1 to 696)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
Tumor Gene Index
Unpublished (1997)

Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapb-r@mail.nih.gov
Tissue procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
The following repetitive elements were found in this cDNA
sequence: 669-696. >GC-rich<Low_complexity
Seq primer: M13 FORWARD
POLA-res.

Location/Qualifiers
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/clone_lib="NCI_CGAP-D10"
/tissue_type="Lung Focal Fibrosis"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a
modified polylinker; Site_1: Ecor I; Site_2: Not I;
NCI_CGAP_D10 is a cDNA library containing the following
tissue(s): A pool of Lung Focal Fibrosis. The library was
constructed according to Bonaldi, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an Ecor I
adaptor, digested with Not I, and cloned directionally
into p773-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
ATACGGCGTG.

| BASE COUNT | 128 a | 244 c | 190 g | 132 t | 2 others |
|---------------------------|--|---|-------|-------|----------|
| ORIGIN | TAG_SEQ-ATACGGGTC* | | | | |
| Query Match | 48.8%; Score 667.8; DB 14; Length 696; | | | | |
| Best Local Similarity | 98.08; Pred. No. 2.4e-154; | | | | |
| Matches 675; Conservative | 0; Mismatches 14; Indels 0; Gaps 0; | | | | |
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| Db | 2 | TTTTTTTTTTTTTTTATCCCTCCTCTTCATTGGTTTAATGTATCGCTACCAACGGTGG | 61 | | |
| Qy | 718 | AAGTCCAAGCTCTACTCCATTGTTGTGGGAAATCGACACCTGAAAGAAGGGGAGCTT | 777 | | |
| Db | 62 | AAGTCCAAGCTCTACTCCATTGTTGTGGGAAATCGACACCTGAAAGAAGGGGAGCTT | 121 | | |
| Qy | 778 | GAAGGAACCTACTAAGCCCTCGGCCCAAAACCAAGCTTTCAGTCCCACTCCAGGCTTC | 837 | | |
| Db | 122 | GAAGGAACCTACTAAGCCCTCGGCCCAAAACCAAGCTTTCAGTCCCACTCCAGGCTTC | 181 | | |
| Qy | 838 | ACCCCCACCCCTGGGCGTTTCAGTCCCGTGGCCCAAGTTTCCACCTTTCAGCTCCAGCTCCACCTAT | 897 | | |

| RESULT 12 | | | | |
|-----------|----------|--------|--------|-----------------|
| BM989994 | | | | |
| LOCUS | BM989994 | 696 bp | linear | EST 17-JUN-2002 |

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12212 row: b column: 02
High quality sequence stop: 654.
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/lab_host="DH10B (phage-resistant)"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."
BASE COUNT 233 a 284 c 262 g 212 t 3 others
ORIGIN
Query Match 47.3%; Score 647.2; DB 14; Length 994;
Best Local Similarity 94.7%; Pred. No. 3.2e-149;
Matches 713; Conservative 0; Mismatches 31; Indels 9; Gaps 4
QY 1 ATGGGCTCTCCACCGTGCCCTGACCTGCTGCTGCGCACTGTGTCTCTGGAGCTTTGGTG 60
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QY 61 GGAATATACCCCTCAGGGGTTATTGGACTGTGTCCTCACCTAGGGACAGGGAGAAGAGA 120
Db 226 GGAATATACCCCTCAGGGGTTATTGGACTGTGTCCTCACCTAGGGACAGGGAGAAGAGA 285
QY 121 GATAGTGTGTGTCACAGGAATATATCCACCTCAAATAATTCGATTTCTGTACC 180
Db 286 GATAGTGTGTGTCACAGGAATATATCCACCTCAAATAATTCGATTTCTGTACC 345
QY 181 AAGTGCACAAAGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGAC 240
Db 346 AAGTGCACAAAGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGAC 405
QY 241 TGCAGGAGTGTGAGAGCGGCTCTTCACCGTTTCAGAAACACACTCAGACACTGCCTC 300
Db 406 TGCAGGAGTGTGAGAGCGGCTCTTCACCGTTTCAGAAACACACTCAGACACTGCCTC 465
QY 301 AGCTGCTCAAATGCCAGAAAGAAATGGTGAGTGGAGATCTTCTTTCACAGTGGAC 360
Db 466 AGCTGCTCAAATGCCAGAAAGAAATGGTGAGTGGAGATCTTCTTTCACAGTGGAC 525
QY 361 CGGGACACCGTGTGGCTGCAGGAAGAACAGTACCGCATATTATGGAGTGAACACCTT 420
Db 526 CGGGACACCGTGTGGCTGCAGGAAGAACAGTACCGCATATTATGGAGTGAACACCTT 585
QY 421 TTCCAGTGTTCAAATGTGACGCTCTGCCTCAATGGGACCGTGCACTCTCCTGCCAGGAG 480
Db 586 TTCCAGTGTTCAAATGTGACGCTCTGCCTCAATGGGACCGTGCACTCTCCTGCCAGGAG 645
QY 481 AAACAGAACACCGTGTGCACTGCGATCGAGTTTCTTTCTTAAGAGAAAACAGTGTGTC 540
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Db 438 TGCAGGAGTGTGAGAGCGGCTCCTTACCGCTTCAGAAAACCACTCAGACACTGCCTC 497
QY 301 AGCTGCTCCAAATGCCGAAAGGAAATGGCTCAGGTGGAGATCTTCTTTCACAGTGGAC 360
Db 498 AGCTGCTCCAAATGCCGAAAGGAAATGGCTCAGGTGGAGATCTTCTTTCACAGTGGAC 557
QY 361 CGGGACACCGTGTGTGGCTGAGGAAAGAACCAAGTACCGGCATTTATTTGGAGTGAACCTT 420
Db 558 CGGGACACCGTGTGTGGCTGAGGAAAGAACCAAGTACCGGCATTTATTTGGAGTGAACCTT 617
QY 421 TTCCAGTCTTCAATTTGAGCCTCTGCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
Db 618 TTCCAGTCTTCAATTTGAGCCTCTGCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 677
QY 481 AAACAGAACACCGTGTGCACCTGCGCATGCGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 540
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QY 541 TCCTGTAGTAAGTGTAAAGAAAGCCTGGAGTGCAGGAAAGTTGTGCTTACCCAGATTGAG 600
Db 738 TCCTGTAGTAAGTGTAAAGAAAGCCTGGAGTGCAGGAAAGTTGTGCTTACCCAGATTGAG 797
QY 601 AATGTTAAGGGCACTGAGGACTCAGGCACCACTGCTGT 640
Db 798 AATGTTAAGGGCACTGAGGACTCAGGCACCACTGCTGT 837
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Search completed: June 9, 2003, 00:13:31
Job time : 1870 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein : nucleic search, using frame_plus_p2n model

Run on: June 8, 2003, 23:42:19 ; Search time 299 Seconds
(without alignments)
3426.954 Million cell updates/sec

Title: US-09-899-422a-2

Perfect score: 2487

Sequence: 1 MGLSTVPDLLPLVLELLV.....DIEELCGPALPPASLLR 455

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool/US09899422/runat_04062003_145736_14694/app_query.fasta_1.647
-DB=N_Geneseq_101002 -OPMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosom62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09899422.ecgn_1.1_396.urnat_04062003_145736_14694 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002.*

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24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|--------|---------------|--------|-------|-------------|
| 1 | 2487 | 100.0 | 1368 | 14 | AAQ49932 |
| 2 | 2487 | 100.0 | 1368 | 21 | AAA95105 |
| 3 | 2487 | 100.0 | 2062 | 13 | AAQ20973 |
| 4 | 2487 | 100.0 | 2062 | 13 | AAQ24440 |
| 5 | 2487 | 100.0 | 2088 | 12 | AAQ10883 |
| 6 | 2487 | 100.0 | 2088 | 22 | AAQ83946 |
| 7 | 2487 | 100.0 | 2111 | 20 | AAQ209170 |
| 8 | 2487 | 100.0 | 2111 | 22 | AAH48859 |
| 9 | 2487 | 100.0 | 2111 | 24 | ABK84039 |
| 10 | 2487 | 100.0 | 2111 | 24 | ABN95862 |
| 11 | 2487 | 100.0 | 2161 | 21 | AAZ48475 |
| 12 | 2487 | 100.0 | 2161 | 24 | ABK13194 |
| 13 | 2487 | 100.0 | 2175 | 16 | AAQ90513 |
| 14 | 2484 | 99.9 | 2111 | 12 | AAQ10955 |
| 15 | 2478 | 99.6 | 2170 | 14 | AAQ50870 |
| 16 | 2471 | 99.4 | 2141 | 11 | AAQ06285 |
| 17 | 2464 | 99.1 | 2176 | 12 | AAQ12215 |
| 18 | 2069 | 83.2 | 1334 | 11 | AAQ06282 |
| 19 | 1563.5 | 62.9 | 2130 | 24 | ABK63694 |
| 20 | 1539.5 | 61.9 | 2173 | 11 | AAQ06284 |
| 21 | 1223.5 | 49.2 | 6889 | 17 | AAV15931 |
| 22 | 1213.5 | 48.8 | 2254 | 21 | AAQ95104 |
| 23 | 1192 | 47.9 | 6926 | 18 | AAV04431 |
| 24 | 1130 | 45.4 | 608 | 13 | AAQ24441 |
| 25 | 1016 | 40.9 | 1301 | 18 | AAQ94022 |
| 26 | 995.5 | 40.0 | 1147 | 18 | AAQ94021 |
| 27 | 992 | 39.9 | 1478 | 20 | AAQ58150 |
| 28 | 946 | 38.0 | 504 | 13 | AAQ24445 |
| 29 | 941 | 37.8 | 483 | 19 | AAV1548 |
| 30 | 941 | 37.8 | 483 | 19 | AAV19801 |
| 31 | 941 | 37.8 | 483 | 20 | AAV81732 |
| 32 | 941 | 37.8 | 483 | 22 | AAQ83945 |
| 33 | 870.5 | 35.0 | 1202 | 18 | AAQ94008 |
| 34 | 854.5 | 34.4 | 477 | 13 | AAQ24444 |
| 35 | 852 | 34.3 | 1049 | 18 | AAQ94007 |
| 36 | 840 | 33.8 | 462 | 13 | AAQ24443 |
| 37 | 840 | 33.8 | 474 | 13 | AAQ24442 |
| 38 | 809 | 32.5 | 1358 | 21 | AAA95103 |
| 39 | 790 | 31.8 | 507 | 24 | ABL99490 |
| 40 | 767.5 | 30.9 | 1977 | 24 | ABA99913 |
| 41 | 766.5 | 30.8 | 5870 | 21 | AAAL5044 |
| 42 | 756.5 | 30.4 | 1674 | 21 | AAQ50196 |
| 43 | 638 | 25.7 | 339 | 19 | AAV19804 |
| 44 | 621 | 25.0 | 333 | 19 | AAV19805 |
| 45 | 615 | 24.7 | 332 | 19 | AAV19803 |

ALIGNMENTS

RESULT 1

AAQ49932

ID AAQ49932 standard; CDNA to mRNA; 1368 BP.

XX XX AAQ49932;

XX AC AAQ49932;

XX DT 29-APR-1994 (first entry)

XX DE XX

XX DE XX

XX DE XX

XX DE XX

XX DE XX

XX DE XX

XX DE XX

XX DE XX

Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor; IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria; rheumatoid arthritis; diabetes; multiple sclerosis; septic shock; pulmonary fibrosis; silicosis; allograft; xenograft; rejection; graft versus host disease; sepsis; inflammation; allergy; autoimmune dysfunction; ss.

OS Homo sapiens.


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Db 361 CCGGACACCGTGTGGCTGCGAGGAAGAACACCGATACCGCATATTGGAGTGAACACCTT 420
QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
Db 421 TTCCAGTGTCTCAATTGACGCTCGCTCAATGGAGCCGTCACCTCTCTCTCCGAGGAG 480
QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
Db 481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTCTTCTTCTAAGAGAAACAGTGTGTC 540
QY 181 SerCysSerAsnCysAlaCysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
Db 541 TCCTGTAGTAACTGTAAAGAAAGCCCTGGAGTGCAGAGTTGTGCTACCCAGATTGAG 600
QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
Db 601 AATGTTAAGGGCACTGAGGACTCAGGACCCAGACGCTGTGCTGCTGCTGCTTCTT 660
QY 221 GlyLeuCysLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
Db 661 GGTCTTTGCTTTTATCCCTCTCTCTCATTTGTTTAAATGATATCGTACCAAGGTGGAAG 720
QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu 260
Db 721 TCCAGCTCTACTCTCATTTGTTGGGAANTCGACACCTGAAAGAGGGGAGCTTGAA 780
QY 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
Db 781 GGAACCTACTACTAAGCCCTGCTGCCCAACCCAGCTTCAGTCCCACTCCAGCTTCACC 840
QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr 300
Db 841 CCCACCTCGGGTTCAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly 320
Db 901 CCGGTGACTGTCCCACTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
Db 961 GCTGACCCCATCTTGGCAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
Db 1021 TGGGAGGACAGCCGACCAAGCCACAGAGCCCTAGACACTGATGACCCGCGAGCTGTAC 1080
QY 361 AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeu 380
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Db 1141 AGCGACACAGAGATCGATCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 401 TyrSerMetLeuAlaThrTrpArgArgThrProArgArgGluAlaThrLeuGluLeu 420
Db 1201 TACACATGCTGGCCACCTGGAGCGGCGCGACGCGCGCGAGGCGGAGCCACGCTGAGGTG 1260
QY 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
Db 1261 CTGGAGCGGTGCTCCGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
Db 1321 CTTTGGCGCGCGCGCGCTCCCGCGCGCGCGCTCTCTCAGA 1365
RESULT 3
AAQ20973
ID AAQ20973 standard; DNA; 2062 BP.
XX AC
XX AAQ20973;
```

```
DT 11-MAY-1992 (first entry)
XX TNF-alpha binding protein gene.
KW Tumour necrosis factor alpha; autoimmune diseases; cachectin; ss;
  extracellular domain.
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 155..1522
FT sig_peptide /*tag= a
FT mat_peptide /*tag= b
FT misc_feature /*tag= c
FT misc_feature /*tag= d
FT misc_feature /*note= 'homologous to probe AAQ20974'
FT misc_feature 242..751
FT misc_feature /*tag= e
FT misc_feature /*note= 'encodes the extracellular domain of human
  TNF alpha receptor'
XX GB2246569-A.
XX 05-FEB-1992.
XX 15-JUN-1990; 90GB-0013410.
XX 15-JUN-1990; 90GB-0013410.
XX (CHAR-) CHARING CROSS SUNLE.
XX Feldman M, Gray P, Turner M, Brennan F;
XX WPI; 1992-043613/06.
XX P-PSDB; AAR20787.
XX New tumour necrosis factor alpha binding protein and polypeptide
  - useful in treating cachexia, sepsis and autoimmune diseases
  e.g. rheumatoid arthritis
XX Disclosure; Fig 1; 25pp; English.
XX The sequence is that of DNA encoding tumour necrosis factor alpha
  binding protein which was obtd. from a human placental cDNA library
  in lambda gt11 using a probe (AAQ20974). The DNA also encodes the
  extracellular domain of human TNF alpha receptor and as such it is
  useful for treating diseases where TNF alpha is involved as a
  causative agent, e.g. cachexia, sepsis and autoimmune diseases,
  specifically rheumatoid arthritis. See also AAQ20974.
XX Sequence 2062 BP; 429 A; 616 C; 573 G; 444 T; 0 other;
Alignment Scores:
Pred. No.: 2,92e-174 Length: 2062
Score: 2487.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-899-422A-2 (1-455) x AAQ20973 (1-2062)
QY 1 MetGlyLeuSerThrValProAspLeuLeuLeuValLeuLeuVal 20
Db 155 ATGGGCTCTCCACCGTCCCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 214
QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGlyLysArg 40
Db 215 GGATATACCCCTCAGGGGTTATTGACTGCTCCTCCTACCTAGGGGACGGAGGAGAGA 274
```

QY 41 AspSerValCysProGlnGlyTyrTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
 DB 275 GATAGTGTGTCTCCCAAGGAAATATATCCACCTCAAAATATTCGATTGTGTATCC 334
 QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
 DB 335 AAGTGCACAAAGGAACCTACTTGTACATGACTGTCCAGGCCCGGGCAGGATACGAC 394
 QY 81 CysArgGluCysGluSerGlySerPheThrLaserGluAsnHisLeuArgHisCysLeu 100
 DB 395 TCCAGGGAGTGTGAGAGGGCTCTTCACCGCTTCAGAAACACCACTCAGACACTGCCTC 454
 QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
 DB 455 AGCTGCTCCAAATGCCGAAGAAATGGTCCAGTGGAGATCTCTTCTGCACAGTGGAC 514
 QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
 DB 515 CGGGACACCGTGTGGCTGCAGGAAGAACCACTACCGCATTTATGGAGTGAAACCTT 574
 QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
 DB 575 TTCCAGTGTCTCAATGTGAGCCTCTGCCTCAATGGAGCCGTGCACCTCTCTCTGCCAGGAG 634
 QY 161 LysGlnAsnThrValCysThrCysHisLaglyPhePheLeuArgGluAsnGluCysVal 180
 DB 635 AAACAGACACCGTGTGCACCTGCCATGCAGGTTCTTCTTAAGAGAAACAGGTGTCTC 694
 QY 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
 DB 695 TCCTGTAGTAACTGTAAAGAAAGCCTGGAGTGCAGCAAGTGTGCTACCCAGATTGAG 754
 QY 201 AsnValLysGlyThrGluAspSerGlyThrValLeuLeuLeuProLeuValIlePhePhe 220
 DB 755 AATGTTAAGGGCACTCAGCACTCAGGCACCACTGCTGTGCTCCCTGCTCATTTTCTTT 814
 QY 221 GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrClnArgTrpLys 240
 DB 815 GGTCTTTGCTTTTATCCCTCTCTCATGTGTTTAATGTATCGTACCAACGGTGGAG 874
 QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGlyLysGluGlyGluLeuGlu 260
 DB 875 TCCAAGCTACTCTCCATTGTTGTGGAAATCGACACCTGAAAGAGGGGAGGCTTGA 934
 QY 261 GlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
 DB 935 GGAACCTACTACTAAGCCCTGCGCCCAACCAACCAAGCTTCAGTCCCACTCCAGCTTCACC 994
 QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerThrThrThr 300
 DB 995 CCCACCTGGGCTTCAGTCCCTGCGCCAGTTCACCTTCACCTCCAGCTCCACCTATAC 1054
 QY 301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly 320
 DB 1055 CCCGTTGACTGTCCCAACTTTGCGGCTCCCGCAGAGGTGGCACCACCTATCAGGG 1114
 QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
 DB 1115 GCTGACCCCTCTTGGCAGAGCCCTGCGCTCCGACCCCAACCCCTTCAGAA 1174
 QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
 DB 1175 TGGGAGGACAGTGGCCACAGCCACAGAGCCCTAGACACTGTAGCCCCCGCAGCTGTAC 1234
 QY 361 AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeu 380
 DB 1235 GCGGTGGTGGAGACGTGCCCCGTTCGCTGGAGGAATTCGTGGGGCCCTAGGGCTG 1294
 QY 381 SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
 DB 1295 AGCGACACAGAGATCGATCGGTGGAGCTGTCAGAACGGCGCTGCTCGCGGAGGCGCAA 1354
 QY 401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420

DB 1355 TACACATGCTGGGACCTGGAGCGGCGACGCGCGCGGCGGCGGCGGCGGCGGCTGAGCTG 1414
 QY 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAla 440
 DB 1415 CTGGGACGCGTGTCCGCGACATGACCTGCTGGGCTGCTGGAGACATCCAGAGGCG 1474
 QY 441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
 DB 1475 CTTTGGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCTCTTCTCAGA 1519

RESULT 4
 AAQ24440
 ID AAQ24440 standard; DNA; 2062 BP.
 XX
 AC AAQ24440;
 XX
 DT 05-NOV-1992 (first entry)
 XX
 DE Encodes TNF-alpha 55KD receptor.
 XX
 KW tumour necrosis factor alpha; extracellular binding domain;
 KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
 KW malaria; viral meningitis; graft versus host disease;
 KW autoimmune disease; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 156..1517
 FT /tag- a
 FT /product= human TNF-alpha
 FT mat_peptide 1265..1267
 FT /tag- b
 FT /note= "3"
 FT mat_peptide 1265..1267
 FT /tag- c
 FT /codon= seq:"TCG", aa:Thr
 FT mat_peptide 1258..1260
 FT /tag- d
 FT /codon= Seq"AAG", aa:Leu
 FT mat_peptide 1433..1435
 FT /tag- e
 FT /codon= Seq:"GAC", aa:Asn
 FT sig_peptide 156..274
 FT /tag- f
 XX
 PN WO207076-A.
 XX
 PD 30-APR-1992.
 XX
 PF 18-OCT-1991; 91WO-GB01826.
 XX
 PR 18-OCT-1990; 90GB-0022648.
 XX
 PA (CHAR-) CHARING CROSS SUNLEY RES CENT.
 XX
 PI Brennan FM, Feldmann M, Gray PW, Turner MJC;
 XX
 DR WPI: 1992-167156/20.
 XX
 DR P-PSDB; AAR24000.
 XX
 DR New polypeptide capable of binding human TNF alpha - comprises
 PT first three cysteine-rich subdomains of TNF alpha receptor for
 PT treating autoimmune disease, septic shock, HIV etc.
 XX
 PS Claim 4; Fig 1; 43pp; English.
 XX
 CC This sequence encodes human TNF-alpha 55kd receptor . A placenta cDNA
 CC library in gt10 was screened with probe AAQ29236. Ten hybridising clones
 CC were plaque purified and cDNA size determined by PAGE against an
 CC Eco RI digested phage DNA. The inserts of two cDNA clones were then
 CC sequenced. The coding region of the majority of the human TNF-alpha

| | |
|------------------------|---|
| RESULT 8 | |
| AAH48859 | |
| ID | AAH48859 standard; DNA; 2111 BP. |
| AC | |
| AAH48859; | |
| XX | |
| DT | 12-NOV-2001 (first entry) |
| XX | |
| DE | Human TNFBP-associated DNA #1. |
| XX | |
| TNF; | tumor necrosis factor binding protein; TNFBP; treatment; |
| KW | insoluble protein; antiinflammatory; immunosuppressive; antibacterial; |
| KW | antiprotozoal; treatment; meningococcal sepsis; cerebral malaria; |
| KW | autoimmune glomerulonephritis; ds. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| FH | |
| FT | Key |
| FT | CDS |
| FT | 187..1554 |
| FT | /*tag= a |
| FT | /product= "TNFBP-associated protein" |
| FT | 187..270 |
| FT | /*tag= b |
| FT | mat_peptide |
| FT | 271..1551 |
| FT | /*tag= c |
| XX | |
| PN | EP132471-A2. |
| XX | |
| PD | 12-SEP-2001. |
| XX | |
| PF | 31-AUG-1990; 2001EP-0108117. |
| XX | |
| PR | 12-SEP-1989; 89CH-0003319. |
| PR | 08-MAR-1990; 90CH-0000746. |
| PR | 20-APR-1990; 90CH-0001347. |
| PR | 31-AUG-1990; 90EP-0116707. |
| PR | 31-AUG-1990; 99EP-0100703. |
| XX | |
| PA | (HOF) HOFFMANN LA ROCHE & CO AG F. |
| XX | |
| PI | Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H; |
| PI | Schlaeger E; |
| XX | |
| DR | WPI; 2001-559312/63. |
| DR | P-PSDB; AAB86817. |
| XX | |
| PT | New homogeneous, insoluble proteins that bind tumor necrosis factor |
| PT | (TNF), useful for treating TNF-mediated disorders, e.g. inflammation |
| XX | |
| PS | Claim 4a; Fig 1; 26pp; German. |
| XX | |
| CC | This invention describes novel insoluble proteins (I), also their |
| CC | (in)soluble fragments and pharmaceutically acceptable salts, able to bind |
| CC | tumor necrosis factor (TNF) and in homogeneous form. The products of the |
| CC | invention have antiinflammatory, immunosuppressive, antibacterial, |
| CC | antiprotozoal activity. (I), and related recombinant proteins, are used |
| CC | to treat diseases mediated by TNF, e.g. shock in cases of meningococcal |
| CC | sepsis; development of autoimmune glomerulonephritis and cerebral |
| CC | malaria. Also (I), or antibodies specific for them, are used for |
| CC | diagnostic determination of TNF in body fluids, for affinity purification |
| CC | of TNF and for identifying (ant)agonists of TNF. This sequence encodes a |
| CC | human TNF binding protein described in the method of the invention. |
| XX | |
| SQ | Sequence 2111 BP; 447 A; 627 C; 587 G; 450 T; 0 other; |
| XX | |
| Alignment Scores: | |
| Pred. No.: | 3e-174 |
| Score: | 2487.00 |
| Percent Similarity: | 100.00% |
| Best Local Similarity: | 100.00% |
| Query Match: | 100.00% |
| DB: | 22 |
| | Gaps: 0 |
| | Indels: 0 |
| | Mismatches: 0 |
| | Conservative: 455 |
| | Matches: 2111 |
| | Length: |

QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
 DB CGGGACACCGTGTGTGGCTGCAGGAAGAACACCGATACCGCATATTGGAGTGAACACCTT 606
 QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
 DB TYCCAGTGTCTCAATTGCAAGCTCTGCCCTCAATGGGACCGTGCACCTCTCCCTGCCAGGAG 666
 QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
 DB AAACAGAACACCGTGCACCTGCCATGCAGGTCTTCTTCTAAGAGAAACACGATGTGTC 726
 QY 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
 DB TCTGTGTAGTAACCTGAAGAAAGCCTGAGTGCAGTGCACGAAGTGTGCTACCCAGATTGAG 786
 QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
 DB AATGTTAAGGGCACTGAGGACTCAGGACCAACAGTGTGTGCCCTGTGCTCATTTCTTTT 846
 QY 221 GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
 DB GGTCTTTGCTTTTATCCCTCTCTTCATTGTTTAAATGATATGCTTACCAACGGTGGAG 906
 QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu 260
 DB TCCAGCTCTACTCCATTGTTGTGGAAATCGACACCTGAAAGAGGGGAGCTTGAA 966
 QY 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
 DB GGAACATACCTACCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1026
 QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrThrThr 300
 DB CCCACCTGGCTTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1086
 QY 301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly 320
 DB CCGGTGTACTTCCCAACTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
 QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
 DB GCTGACCCCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1206
 QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
 DB TGGGAGGACAGCGCCACAGCCACAGAGAGCTAGACACTCATGCCCGGAGCGCTGTAC 1266
 QY 361 AlaValValGluAsnValProProLeuArgTrpPlyGluPheValArgArgLeuGlyLeu 380
 DB GCCGTGTGTGAGAACGTGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326
 QY 381 SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
 DB AGGACACAGAGATCATCGCTGGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1386
 QY 401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420
 DB TACAGCATGCTGGCAGCTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1446
 QY 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
 DB CTGGGACGGCTGCTCGCGACATGAGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1506
 QY 441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
 DB CTTTGG 1551
 1507 CTTTGG

RESULT 11

AAZ48475

ID AAZ48475 standard; DNA; 2161 BP.

XX

AC AAZ48475;
 XX 31-MAR-2000 (first entry)
 DE Human tumour necrosis factor receptor (TNFR1) nucleotide sequence.
 XX Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;
 KW Inflammation; tumour formation; TNFR1; anticancer; ds.
 XX Homo sapiens.
 OS
 XX US6007995-A.
 PN
 XX 28-DEC-1999.
 PD
 XX 26-JUN-1998; 98US-0106038.
 PF
 XX 26-JUN-1998; 98US-0106038.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Baker BF, Cowseert LM;
 XX WPI; 2000-105333/09.
 DR
 XX
 XX Antisense inhibition of tumor necrosis factor type 1 expression for
 PT diagnosis, treatment and prevention of disease, particularly tumors
 PS Example 10; Columns 33-36; 34pp; English.
 XX The invention provides antisense compounds targeted to human tumour
 CC necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds
 CC can be used in a method of inhibiting the expression of TNFR1 human cells
 CC or tissues. The antisense compounds specifically hybridize with one or
 CC more nucleic acids encoding TNFR1 modulating the function of nucleic
 CC acid molecules encoding TNFR1, ultimately modulating the amount of TNFR1
 CC produced. The antisense compounds and method are useful as research
 CC reagents and diagnostics, and in the treatment and prophylaxis of
 CC infection, inflammation or tumour formation. The present sequence
 CC represents the nucleotide sequence of human TNFR1 (GenBank Accn No:
 CC X55313).
 XX
 SQ Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other;
 Alignment Scores:
 Pred. No.: 3,1e-174 Length: 2161
 Score: 2487.00 Matches: 455
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0
 US-09-899-422a-2 (1-455) x AAZ48475 (1-2161)
 QY 1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuGluLeuVal 20
 DB 256 ATGGGGCTCTCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315
 QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyArgGluLysArg 40
 DB 316 GGAATATACCCCTCAGGGGTATTGGACTGGTCCCTCACCCTGAGGAGGAGAGAGA 375
 QY 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 60
 DB 376 GATAGTGTGTGTCCTCCCAAGGAATATATATCCACCTCANNATATTCGATTGCTGTACC 435
 QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyGlnAspThrAsp 80
 DB 436 AAGTGCACAAAGGAACCTACTTGTACATGACTGTCCAGCGCCGGGACAGGAC 495
 QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
 DB 496 TGCAGGGAGTGTGAGAGCGGCTCTCTTCCCGCTTCAGAAAACACCTCAGACACTGCCTC


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Oy 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
Db 556 AGCTGCTCCAAATGCCGAAGAAATGGTCAGGTGGAGATCTCTTTCACAGTGGAC 615
Oy 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyArgHisTyTrpSerGluAsnLeu 140
Db 616 CGGGACACCGTGCTGGCTGCAGGAAGAACAGTACCGGCATTATTGGAGTGAACCTT 675
Oy 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
Db 676 TTCAGTGCTTCATTTGACGCTCTGCTCAATGGGACCGTGCACCTCTCTCCAGGAG 735
Oy 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
Db 736 AAACAGAACACCGTGTGCACCTGCCATGCCAGTTCCTTCTAAGAGAAACAGAGTGTGC 795
Oy 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
Db 796 TCTGTGTAGTAACCTGTGAAGAAAGCCCTGGAGTGCAGGAAGTGTGCTACCCAGATTGAG 855
Oy 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
Db 856 AATGTTAAGGCACTAGGACCTCAGGACACACAGTCTGTGCTCCCTGTGCTATTTCTTT 915
Oy 221 GlyLeuCysLeuSerLeuPheIleGlyLeuMetTyArgTyArgTrpLys 240
Db 916 GGTCTTTGGCTTTTATCCCTCTCTCTTCAATTGTTTAAATGATGCTACCAACGGTGGAG 975
Oy 241 SerLysLeuTySerIleValCysGlyLysSerThrProGluLysGluGluLeuGlu 260
Db 976 TCCAGCTCTACTCCATTTGTTGGAAATGCACACCTGAAAGAGGGGAGCTTGA 1035
Oy 261 GlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
Db 1036 GGAACCTACTAAGCCCTGCCCCCAACCAAGCTTCAGTCCCACTCCAGGCTCAC 1095
Oy 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerThrTyThr 300
Db 1096 CCCAGCTGGGCTTCAGTCCCTGCTCCAGTTCACCTTCACCTCCAGCTCCACCTATACC 1155
Oy 301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyroGlnGly 320
Db 1156 CCGGTGACTGTCCCACTTTGCGGCTCCCGCAGAGAGTGGCACCACTTATCAGGGG 1215
Oy 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
Db 1216 GCTGACCCCATCTTGCAGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAG 1275
Oy 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTy 360
Db 1276 TGGGAGGACAGCGCCCAAGCCACAGAGCCTAGACACTGATGACCCCGCAGCGTGTAC 1335
Oy 361 AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeu 380
Db 1336 CCGGTGGTGGAGAGCTGCCCTGCTGGAGGAATTCGTGCGCGCTAGGGGTG 1395
Oy 381 SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
Db 1396 AGCGACCAACGAGATCGATCGCTGGAGCTGCAGAGCGGCGCTGCTGCGCGAGCGGCA 1455
Oy 401 TyrSerMetLeuAlaThrTrpArgArgThrProArgArgGluAlaThrLeuGluLeu 420
Db 1456 TACAGCATGCTGGGACCTGGAGCGGCGCACCGCGCGGCGGAGCCACGCTGGAGCTG 1515
Oy 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
Db 1516 CTGGACCGGTGCTCCCGCATGGACTGCTGGGCTGCTGGAGGACATGAGGAGGCG 1575
Oy 441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
Db 1576 CTTTGGCGCGCGCGCGCTCCCGCGCGCGCGCGCTTCTTCAGA 1620

```

RESULT 12
ABK13194

ID ABK13194 standard; DNA; 2161 BP.

XX

AC ABK13194;

XX

DT 23-APR-2002 (first entry)

XX

DE Human tumour necrosis factor alpha (TNF alpha) receptor DNA.

XX

TNF alpha; apoptosis; ds; tumour; death domain receptor ligand; diterpenoid triepoxide; cytostatic activity; c-IAP2; c-IAP1; carcinoma; mammary adenocarcinoma; non-small cell lung carcinoma; neurological malignancy; haematological malignancy; lichen planus; non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic; malignant cutaneous T-cell lymphoma; mycosis fungoides; anti-metastatic; non-NF cutaneous T-cell lymphoma; mycosis fungoides; anti-tumour; T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid; discoid lupus erythematosus; human; gene; receptor; TNF-R1.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 256..1623

FT

FT /*tag- a "TNF alpha protein"

XX

PN US6329148-B1.

XX

PD 11-DEC-2001.

XX

PF 15-FEB-2000; 2000US-0505250.

XX

PR 16-FEB-1999; 99US-120313P.

XX

PR 20-AUG-1999; 99US-149989P.

XX

PA (STRD) UNIV LELAND STANFORD.

XX

PI Rosen GD, Kao P;

XX

DR WPI; 2002-121125/16.

XX

DR P-PSDB; AAU75064.

XX

PT Use of a synergistic combination of death domain receptor ligands and diterpenoid triepoxides for killing of tumour cells -

XX

PS Disclosure; Column 23-28; 20pp; English.

XX

This invention relates to a novel method for enhanced killing of tumour cells comprising contacting a tumour cell with a synergistic combination of a death domain receptor ligand and a diterpenoid triepoxide. This method has cytostatic activity and works by blocking TNF-alpha mediated induction of c-IAP2 and c-IAP1. The method of the invention may be used for treating tumours, particularly solid tumours, e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma also neurological malignancies, haematological malignancies, e.g. non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, malignant cutaneous T-cells, mycosis fungoides, non-MF cutaneous T-cell lymphoma, lymphomatoid papulosis, T-cell rich cutaneous lymphoid hyperplasia, bullous pemphigoid, discoid lupus erythematosus, lichen planus. The combination may be administered with other active agents, e.g. anti-metastatic, anti-tumour or anti-angiogenic agents. The potent synergy between the diterpenoids and the death domain ligands allows increased killing at equivalent or lower doses, and can sensitise otherwise resistant cells. This sequence represents the human tumour necrosis factor alpha receptor (TNF-R1) DNA. TNF-R1 is a death domain receptor used in the used method of the invention in combination with diterpenoid triepoxides to kill tumours by inducing apoptosis.

XX

SO Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other;

XX

Alignment Scores:

Pred. No.: 3.1e-174 Length: 2161

| | | | |
|-----------|---|--|------|
| Db | 1216 | GCTGACCCCATCTTGGAGACAGCCCTCGCTCGACCCCATCCCAACCCCTTCAGAAG | 1275 |
| Qy | 341 | TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr | 360 |
| Db | 1276 | TGGGAGACAGCGCCACAGCCACAGAGCTAGACACTGATGACCCCGGACGCTGTAC | 1335 |
| Qy | 361 | AlaValValGluAsnValProProLeuArgTrpIlyGluPheValArgArgLeuGlyLeu | 380 |
| Db | 1336 | GCCTGTGTGAGAACGTGCCCGTTGCGCTGGAAGAAATTCGTGCGCGCTAGGCGTG | 1395 |
| Qy | 381 | SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln | 400 |
| Db | 1396 | AGCGACACAGAGATCGATCGCTGGAGCTGCAGAACGGGGCTGCTTGCAGGCGCAA | 1455 |
| Qy | 401 | TyrSerMetLeuAlaThrTrpAspArgArgThrProArgArgGluAlaThrLeuGluLeu | 420 |
| Db | 1456 | TACAGCATGCTGGCGACTGGAGCGGGCGACGCGCGGGCGGAGCCAGCTGGAGCTG | 1515 |
| Qy | 421 | LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAla | 440 |
| Db | 1516 | CTGGAGCGCTGTCTCCGACATGAGCTGTGGCTGCCTGGAGGACATCGAGGAGCG | 1575 |
| Qy | 441 | LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg | 455 |
| Db | 1576 | CTTTGCGCGCGCGCGCTCCCGCGCGCCAGCTTCTCAGA | 1620 |
| RESULT 13 | | | |
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| ID | AAQ90513 standard; DNA; 2175 BP. | | |
| XX | AAQ90513; | | |
| XX | AC | | |
| XX | 19-JAN-1996 (first entry) | | |
| XX | p55 TNF-R gene. | | |
| DE | | | |
| XX | p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera; | | |
| KW | epidermal growth factor receptor; EGF-R; protease; inhibitor; | | |
| KW | phorbol myristate acetate; PMA; ss. | | |
| XX | Homo sapiens. | | |
| XX | | | |
| Key | Location/Qualifiers | | |
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| CDS | /*tag= a | | |
| FT | /product= p55 TNF-R | | |
| FT | 2143..2149 | | |
| FT | /*tag= b | | |
| FT | /note= "possible poly-A signal" | | |
| FT | | | |
| XX | A09475742-A. | | |
| PN | | | |
| XX | | | |
| PD | 04-MAY-1995. | | |
| XX | | | |
| PF | 11-OCT-1994; 94AU-0075742. | | |
| XX | | | |
| PR | 12-OCT-1993; 93IL-0107268. | | |
| XX | | | |
| PA | (YEDA) YEDA RES & DEV CO LTD. | | |
| XX | | | |
| PI | Batkin M, Brakebusch C, Varfolomeev E, Wallach D; | | |
| XX | | | |
| DR | WPI; 1995-194342/26. | | |
| DR | P-PSDB; AAR75084. | | |
| XX | | | |
| PT | New protease capable of cleaving soluble tumour necrosis factor | | |
| PT | (TNF) receptor - from cell-bound TNF- receptor, useful for | | |
| PT | antagonising deleterious effects of TNF. | | |
| XX | | | |
| PS | Disclosure; Fig 1; 40pp; English. | | |
| XX | | | |
| CC | This sequence represents human p55tumour necrosis factor (TNF-R) DNA. | | |

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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2003, 20:42:48 ; Search time 344 Seconds
(without alignments)
8955.621 Million cell updates/sec

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Perfect score: 1368

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Scoring table: IDENTIFY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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|------------|--------|-------------|--------|----|-------------|
| 1 | 1366.4 | 99.9 | 1368 | 14 | AAQ49932 |
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| 3 | 1366.4 | 99.9 | 2088 | 12 | AAQ10883 |
| 4 | 1366.4 | 99.9 | 2088 | 22 | AAQ83946 |
| 5 | 1366.4 | 99.9 | 2111 | 20 | AAQ09170 |
| 6 | 1366.4 | 99.9 | 2111 | 22 | AAH48859 |
| 7 | 1366.4 | 99.9 | 2111 | 24 | ABK84039 |
| 8 | 1366.4 | 99.9 | 2111 | 24 | ABN95862 |
| 9 | 1366.4 | 99.9 | 2161 | 21 | AAZ48475 |

| | | | | | | |
|----|--------|------|------|----|-----------|---------------------|
| 10 | 1366.4 | 99.9 | 2161 | 24 | ABK13194 | Human tumour necro |
| 11 | 1364.8 | 99.8 | 2111 | 12 | AAQ10955 | Encodes human 55kD |
| 12 | 1364.8 | 99.8 | 2175 | 16 | AAQ05113 | p55 TNF-R gene. H |
| 13 | 1363.2 | 99.6 | 2062 | 13 | AAQ20973 | TNF-alpha binding |
| 14 | 1363.2 | 99.6 | 2062 | 13 | AAQ24440 | Encodes TNF-alpha |
| 15 | 1363.2 | 99.6 | 2176 | 12 | AAQ12215 | Type I TNF receptor |
| 16 | 1361.6 | 99.5 | 2141 | 11 | AAQ06285 | Human Tumour Necro |
| 17 | 1360 | 99.4 | 2170 | 14 | AAQ050870 | p55 Tumour necrosi |
| 18 | 1120.4 | 81.9 | 1334 | 11 | AAQ06282 | Plasmid Tumour Nec |
| 19 | 743.4 | 54.3 | 2130 | 24 | ABK63694 | Rat sequence diffe |
| 20 | 732.2 | 53.5 | 2173 | 11 | AAQ06284 | Rat Tumour Necrosi |
| 21 | 632.8 | 46.3 | 6926 | 18 | AAV04431 | Vector pcDNA3-1961 |
| 22 | 632.4 | 46.2 | 6889 | 17 | AAV15931 | DRFR/Intron (WTRs |
| 23 | 515.4 | 43.6 | 608 | 13 | AAQ24441 | Encodes truncated |
| 24 | 515.4 | 37.7 | 1478 | 20 | AAQ58150 | CadC-fusion polytpe |
| 25 | 514 | 37.6 | 1301 | 18 | AAQ94022 | CDNA for TBP(20-19 |
| 26 | 506 | 37.0 | 1147 | 18 | AAQ94021 | CDNA for TBP(20-19 |
| 27 | 501.4 | 36.7 | 504 | 13 | AAQ24445 | Encodes truncated |
| 28 | 483 | 35.3 | 483 | 19 | AAV41548 | Human soluble tumo |
| 29 | 483 | 35.3 | 483 | 19 | AAV19801 | Soluble tumour nec |
| 30 | 483 | 35.3 | 483 | 20 | AAV81732 | Tumour necrosis in |
| 31 | 483 | 35.3 | 483 | 22 | AAV83945 | Human 30 kDa TNF 1 |
| 32 | 440 | 32.2 | 2254 | 21 | AAQ95104 | partial human TNFR |
| 33 | 424.4 | 31.0 | 1049 | 18 | AAQ94007 | CDNA for TBP(20-16 |
| 34 | 424.4 | 31.0 | 1202 | 18 | AAQ94008 | CDNA for TBP(20-16 |
| 35 | 418 | 30.6 | 1674 | 21 | AAZ50196 | Male fusion plasm |
| 36 | 381 | 27.9 | 1977 | 24 | ABA99913 | TNF-selectokine pr |
| 37 | 376.2 | 27.5 | 477 | 13 | AAQ24444 | Encodes truncated |
| 38 | 375.8 | 27.5 | 507 | 24 | ABL99490 | Target canine gene |
| 39 | 357.2 | 26.1 | 474 | 13 | AAQ24442 | Encodes truncated |
| 40 | 329.6 | 24.1 | 5870 | 21 | AAV15044 | Nucleotide sequenc |
| 41 | 312.4 | 22.8 | 339 | 19 | AAV19804 | Truncated stNFR, s |
| 42 | 310.8 | 22.7 | 462 | 13 | AAQ24443 | Encodes truncated |
| 43 | 308.2 | 22.5 | 333 | 19 | AAV19805 | Truncated stNFR, s |
| 44 | 304.4 | 22.3 | 332 | 19 | AAV19803 | Truncated stNFR, s |
| 45 | 294.6 | 21.5 | 315 | 19 | AAV19806 | Truncated stNFR, s |

ALIGNMENTS

RESULT 1

AAQ49932
ID AAQ49932 standard; CDNA to mRNA; 1368 BP.

XX AAQ49932;

XX 29-APR-1994 (first entry)

XX Lambda-derived TNF-R CDNA.

XX Human; tumour necrosis factor receptor; TNF-R; Interleukin-1 receptor;
KW IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW graft versus host disease; sepsis; inflammation; allergy;
KW autoimmune dysfunction; ss.
XX Homo sapiens.
OS Lambda-gt10-7-ctnfbp.

| Key | Location/Qualifiers |
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| FT | /product= hTNF-R |
| FT | 1..120 |
| FT | /*tag- b |
| FT | mat_peptide 121..1363 |
| FT | /*tag- c |
| XX | WO9319777-A. |
| PD | 14-OCT-1993. |

XX PF 26-MAR-1993; 93WO-US02938.
 XX PR 30-MAR-1992; 92US-0860710.
 XX PA (IMMV) IMMUNEX CORP.
 XX PI Smith CA;
 XX DR WPI; 1993-336592/42.
 XX DR P-PSDB; AAR42059.
 XX PT New fusion protein tumour necrosis factor and human interleukin-1
 XX PT receptor - useful in therapy, diagnosis and assays of e.g.
 XX PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
 XX PS Disclosure; Page 57-59; 85pp; English.
 XX CC The sequences given in AAQ49931-32 encode human tumour necrosis factor
 XX CC receptor (TNF-R) and the sequences in AAQ49933-34 encode human
 XX CC interleukin-1 receptor (IL-1R). These sequences were used in the
 XX CC production of a fusion protein which conformed to one of the
 XX CC formulae:
 XX CC TNF-R-linker-TNF-R-linker-IL-1R
 XX CC IL-1R-linker-TNF-R-linker-TNF-R or
 XX CC TNF-R-linker-TNF-R-linker-TNF-R
 XX CC The linker may comprise 5-100 amino acids selected from Gly, Asp,
 XX CC Ser, Thr and Ala. These linkers separate the individual moieties
 XX CC by such a distance that each component of the fusion protein is
 XX CC capable of folding into the secondary or tertiary structure required
 XX CC for its biological activity. These fusion proteins may be used in
 XX CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
 XX CC particularly in conditions in which both TNF and IL-1 play a causative
 XX CC role. They may be used to treat cachexia, rheumatoid arthritis,
 XX CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
 XX CC cerebral malaria, allograft and xenograft rejection in graft verses
 XX CC host disease, sepsis, septic shock, inflammation, allergies and
 XX CC autoimmune dysfunctions.

Query Match
 Beat Local Similarity 99.9%; Score 1366.4; DB 14; Length 1368;
 Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ATGGGCTCTCCACCGTCCCTGACCTGCTGCTGCCACTGCTGCTCTGAGCTGTGGTG 60
 DB 1 ATGGGCTCTCCACCGTCCCTGACCTGCTGCTGCCGCTGCTGCTCTGAGCTGTGGTG 60
 OY 61 GGAATATACCCCTCAGGGGTATTGGACTGCTGCTCCTCACCTAGGGGACAGGAGAAGA 120
 DB 61 GGAATATACCCCTCAGGGGTATTGGACTGCTGCTCCTCACCTAGGGGACAGGAGAAGA 120
 OY 121 GATAGTGTGTGTCCTCCAGGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 180
 DB 121 GATAGTGTGTGTCCTCCAGGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 180
 OY 181 AAGTCCCAAGAAACCTACTTGTACAATGACTGTCCAGGCCGGGGCAGGATACGGAC 240
 DB 181 AAGTCCCAAGAAACCTACTTGTACAATGACTGTCCAGGCCGGGGCAGGATACGGAC 240
 OY 241 TCGAGGGAGTGTAGAGGGGCTCTTCCACCTCCTCAGAAACACCTCAGACATGCGCTC 300
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 OY 301 AGCTGTCTCCAAATCCGAAAGAAATGGTCACTGAGTGGAGATCTCTTTCGACAGTGGAC 360
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OY 421 TTCAGTGTCTCAATTTGAGCCTCTGCTCAATGGAGCCGTGACCTCTCTGCGAGGAG 480
 DB 421 TTCAGTGTCTCAATTTGAGCCTCTGCTCAATGGAGCCGTGACCTCTCTGCGAGGAG 480
 OY 481 AACAGAACCCGTGTGCACCTGCCATGCGAGTTCTTCTTAAGAGAAACAGTGTGTC 540
 DB 481 AACAGAACCCGTGTGCACCTGCCATGCGAGTTCTTCTTAAGAGAAACAGTGTGTC 540
 OY 541 TCCTGTAGTAACTGTAAAGAAAGCCTGGAGTGCACAGTTGTGCTACCCAGATTGAG 600
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 OY 601 AATGTTAAGGCACTGAGGACTCAGGACACCAAGTGTGTTGCCCTGCTATTTCTTT 660
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RESULT 2
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 ID AAA95105 standard; DNA; 1368 BP.
 XX AC AAA95105;
 XX DT 12-JAN-2001 (first entry)
 XX


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Db 667 AAACAGAACACCGTGTGCACCTGCCATGCGAGGTTCTTTCTAAGAGAAAACAGTGTGTC 726
QY 541 TCTGTAGTAACTGTAAAGAAAGCCTGGAGTGCACGAAGTTGTGCTACCCAGATTGAG 600
Db 727 TCTGTAGTAACTGTAAAGAAAGCCTGGAGTGCACGAAGTTGTGCTACCCAGATTGAG 786
QY 601 AATGTTAAGGCACCTGAGGACTCAGGCACACAGTGTGTTGCCCTGCTCATTTTCCTTT 560
Db 787 AATGTTAAGGCACCTGAGGACTCAGGCACACAGTGTGTTGCCCTGCTCATTTTCCTTT 846
QY 661 GGTCTTTGCTTTTATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 847 GGTCTTTGCTTTTATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 906
QY 721 TCCAGCTCTACTCCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 780
Db 907 TCCAGCTCTACTCCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 966
QY 781 GGAAGTACTAAGCCCTGCTGCCCAACACCAAGCTTCAGTCCCACTCCAGGCTTCACC 840
Db 967 GGAAGTACTAAGCCCTGCTGCCCAACACCAAGCTTCAGTCCCACTCCAGGCTTCACC 1026
QY 841 CCCACCTGGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 1027 CCCACCTGGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1086
QY 901 CCGGTGACTGCTCCCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 1087 CCGGTGACTGCTCCCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
QY 961 GCTGACCCCATCTTGGGACAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 1147 GCTGACCCCATCTTGGGACAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1206
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RESULT 6

AAH48859

ID AAH48859 standard; DNA; 2111 BP.

XX

AC AAH48859;

XX

DT 12-NOV-2001 (first entry)

XX

DE Human TNFBP-associated DNA #1.

XX

KW TNF; tumor necrosis factor binding protein; TNFBP; treatment;
KW insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
KW antiprotozoal; treatment; meningococcal sepsis; cerebral malaria;
KW autolimmune glomerulonephritis; ds.

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XX Homo sapiens.
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XX Key
FH Location/Qualifiers
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FT /*tag= b
FT 271..1551
FT /*tag= c
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XX EP1132471-A2.
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XX 12-SEP-2001.
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XX 31-AUG-1990; 2001EP-0108117.
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XX 12-SEP-1989; 89CH-0003319.
PR 08-MAR-1990; 90CH-0000746.
PR 20-APR-1990; 90CH-0001347.
PR 31-AUG-1990; 90EP-0116707.
PR 31-AUG-1990; 99EP-0100703.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Brockhaus M, Demblic Z, Gentz R, Lesslauer W, Loetscher H;
PI Schlaeger E;
XX
XX WPI: 2001-559312/63.
DR P-PSDB; AAB6817.
XX
XX New homogeneous, insoluble proteins that bind tumor necrosis factor
PT (TNF), useful for treating TNF-mediated disorders, e.g. inflammation
PS
XX Claim 4a; Fig 1; 26pp; German.
XX
XX This invention describes novel insoluble proteins (I), also their
CC (in)soluble fragments and pharmaceutically acceptable salts, able to bind
CC tumor necrosis factor (TNF) and in homogeneous form. The products of the
CC invention have antiinflammatory, immunosuppressive, antibacterial,
CC antiprotozoal activity. (I), and related recombinant proteins, are used
CC to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
CC sepsis; development of autolimmune glomerulonephritis and cerebral
CC malaria. Also (I), or antibodies specific for them, are used for
CC diagnostic determination of TNF in body fluids, for affinity purification
CC of TNF and for identifying (ant)agonists of TNF. This sequence encodes a
CC human TNF binding protein described in the method of the invention.
XX
XX Sequence 2111 BP; 447 A; 627 C; 587 G; 450 T; 0 other;
QY Query Match 99.9%; Score 1366.4; DB 22; Length 2111;
Db Best Local Similarity 99.9%; Pred. No. 0;
Mismatches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 187 ATGGGCTCTCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 246
QY 61 GGAATATACCCCTCAGGGGTTATTGGACTGCTCCCTCACCTAGGGGACAGGAGAGA 120
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QY 121 GATAGTGTGTGCTCCCAAGGAAATATATCCACCCCTCAAAATATTCGATTGCTGTACC 180
Db 307 GATAGTGTGTGCTCCCAAGGAAATATATCCACCCCTCAAAATATTCGATTGCTGTACC 366
QY 181 AAGTGCACAAAGAACCTTACTTGTACATGCTCCAGGCCCGGGGAGGATACGAC 240
Db 367 AAGTGCACAAAGAACCTTACTTGTACATGCTCCAGGCCCGGGGAGGATACGAC 426
QY 241 TGCAGGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAACACCTCAGACACTGCCTC 300
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Db 427 TGCAGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAACACACCTCAGACACTGCCTC 486
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QY 361 CGGGACACCGTGTGGGTGAGGAGAGAACAGTACCGGCAATTTATGGAGTGAACACCTT 420
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QY 421 TTCAGTGTCAATTTGAGCGCTCTGCTCAATGGGACCGTGCACCTCTCTCTGCCAGGAG 480
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QY 481 AAACAGAACACCGTGTGCACCTGCCATGCAGTGTCTTTTAAAGAGAAAGAGTGTGTC 540
Db 667 AAACAGAACACCGTGTGCACCTGCCATGCAGTGTCTTTTAAAGAGAAAGAGTGTGTC 726
QY 541 TCCTGTAGTAACTGTAGAAAGCGTGGAGTGCAGGAAGTTGTGCTACCCAGATTGAG 600
Db 727 TCCTGTAGTAACTGTAGAAAGCGTGGAGTGCAGGAAGTTGTGCTACCCAGATTGAG 786
QY 601 AATGTTAAGGCACTGAGGACTCAGGCACACAGTGTGTTGCCCTGCTCATTTTCTTT 660
Db 787 AATGTTAAGGCACTGAGGACTCAGGCACACAGTGTGTTGCCCTGCTCATTTTCTTT 846
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QY 721 TCCAGGCTACTCAATTTGTTGGGAATCGACACCTGAAAGAGAGGGAGCTTGAA 780
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QY 901 CCCGCTGCTGCTCACTTTGCGGCTCCCGCAGAGAGTGGCAGCACCTATCAGGG 960
Db 1087 CCCGCTGCTGCTCACTTTGCGGCTCCCGCAGAGAGTGGCAGCACCTATCAGGG 1146
QY 961 GCTGACCCCTCTTGGGACAGCCCTCGCTCCGACCCCACTCCCAACCCCTTCAGAG 1020
Db 1147 GCTGACCCCTCTTGGGACAGCCCTCGCTCCGACCCCACTCCCAACCCCTTCAGAG 1206
QY 1021 TGGGAGGACAGCCGCAAGCCACAGAGCTAGACACTGATGACCCGCGAGCGTGPAC 1080
Db 1207 TGGGAGGACAGCCGCAAGCCACAGAGCTAGACACTGATGACCCGCGAGCGTGPAC 1266
QY 1081 GCGTGTGGAGAGCTGCCCCGCTGCTGCTGGAAGGATTCGTCGCGCGCTTAGGCTG 1140
Db 1267 GCGTGTGGAGAGCTGCCCCGCTGCTGCTGGAAGGATTCGTCGCGCGCTTAGGCTG 1326
QY 1141 AGCCACACAGAGTGCATGCTGCTGAGCTGCAGAACCGGCGCTGCTGCGGAGCGGCA 1200
Db 1327 AGCCACACAGAGTGCATGCTGCTGAGCTGCAGAACCGGCGCTGCTGCGGAGCGGCA 1386
QY 1201 TACAGATGCTGGGACCTGAGAGCGGCGCAGCCGCGGCGAGGCCACGCTGAGCTG 1260
Db 1387 TACAGATGCTGGGACCTGAGAGCGGCGCAGCCGCGGCGAGGCCACGCTGAGCTG 1446
QY 1261 CTGGAGCGCTGCTCCGAGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
Db 1447 CTGGAGCGCTGCTCCGAGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1506
QY 1321 CTTTTCGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
Db 1507 CTTTTCGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1554

RESULT 7

ABK84039

ID ABR84039 standard; cDNA; 2111 BP.

XX ABR84039;

XX 14-AUG-2002 (first entry)

XX Human cDNA differentially expressed in granulocytic cells #610.

Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.

OS Homo sapiens.

XX WO200228999-A2.

XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US30821.

XX 03-OCT-2000; 2000US-237189P.

XX (GENE-) GENE LOGIC INC.

XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX WPI; 2002-435328/46.

Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.

XX Claim 1; SEQ ID No 610; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA.

Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection,


```
QY 961 GCTGACCCCATCTTGGGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAAG 1020
DB 1115 GCTGACCCCATCTTGGGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAAG 1174
QY 1021 TGGGAGGACAGCCGACCAAGCCACAGAGCCCTAGACACTGATGACCCGCGACGCTGTAC 1080
DB 1175 TGGGAGGACAGCCGACCAAGCCACAGAGCCCTAGACACTGATGACCCGCGACGCTGTAC 1234
QY 1081 GCCGTGGTGGAGACGTCGCCCGCTTGGGCTGGAGGAATTCGTGCGCGCCCTAGGCGTG 1140
DB 1235 GCCGTGGTGGAGACGTCGCCCGCTTGGGCTGGAGGAATTCGTGCGCGCCCTAGGCGTG 1294
QY 1141 ACCGACCCAGAGATCGATCGGTGAGCTGCGAGACGGCGCTGCTGGCGAGCGCAA 1200
DB 1295 ACCGACCCAGAGATCGATCGGTGAGCTGCGAGACGGCGCTGCTGGCGAGCGCAA 1354
QY 1201 TACACATGCTGGGACCTGGAGCGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
DB 1355 TACACATGCTGGGACCTGGAGCGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1414
QY 1261 CTGGACGCGTGTCCGCGACATGACCTGCTGGGCTGCTGGAGGACATCGAGAGCGG 1320
DB 1415 CTGGACGCGTGTCCGCGACATGACCTGCTGGGCTGCTGGAGGACATCGAGAGCGG 1474
QY 1321 CTTTGGCGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
DB 1475 CTTTGGCGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1522
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RESULT 14

AAQ24440

ID AAQ24440 standard; DNA; 2062 BP.

XX AC AAQ24440;

XX 05-NOV-1992 (first entry)

DZ Encodes TNF-alpha 55KD receptor.

XX

KW tumour necrosis factor alpha; extracellular binding domain;

KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;

KW malaria; viral meningitis; graft versus host disease;

KW autoimmune disease; rheumatoid arthritis.

XX

OS Homo sapiens.

XX

FH Key

FT CDS

FT

FT Location/Qualifiers

FT 156..1517

FT /*tag= a

FT /product= human TNF-alpha

FT 1265..1267

FT /*tag= b

FT /note= "3"

FT 1265..1267

FT /*tag= c

FT /codon= seq: "TGG", aa: Thr

FT 1258..1260

FT /*tag= d

FT /codon= Seq "AAG", aa: Leu

FT 1433..1435

FT /*tag= e

FT /codon= Seq: "GAC", aa: Asn

FT 156..174

FT /*tag= f

FT

FT

PN W09207076-A.

XX

PD 30-APR-1992.

XX

PD 18-OCT-1991;

XX 91WO-GB01826.

XX

PD 18-OCT-1990;

XX 90GB-0022648.

XX

XX

PA

XX

PI

XX

PI

XX

DR

DR

XX

PT

PT

XX

PT

PT

XX

PS

XX

CC

CC

CC

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CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

(CHAR-) CHARING CROSS SUNLEY RES CENT.

Brennan EM, Feldmann M, Gray PW, Turner MJC;

WPI: 1992-167156/20.

P-PSDB; AAR24000.

New polypeptide capable of binding human TNF alpha - comprises first three cysteine-rich subdomains of TNF alpha receptor for treating autoimmune disease, septic shock, HIV etc.

Claim 4; Fig 1; 43pp; English.

This sequence encodes human TNF-alpha 55KD receptor . A placenta cDNA library in gt10 was screened with probe AAQ29236. Ten hybridising clones were plaque purified and cDNA size determined by PAGE against an Eco RI digested phage DNA. The insert of two cDNA clones were then sequenced. The coding region of the majority of the human TNF-alpha 55KD receptor was isolated as an EcoRI fragment encoding 374 amino acids, and cloned into a mammalian cell expression vector, resulting in pTNFR. A derivative of the TNF-alpha receptor was produced by engineering a termination codon just prior to the transmembrane domain. PCR with primers AAQ29237,8 generated a 300bp restriction fragment which was cloned into pTNFR, giving pTNFRcd. DNA sequencing confirmed this contained the designed DNA sequence. The TNF-alpha receptor expression plasmids were then transfected into monkey COS-7 cells.

See also AAQ24440-51, AAR24000, AAR24080-84, AAR27585, AAQ29236-8

Sequence 2062 BP; 429 A; 618 C; 572 G; 443 T; 0 other;

Query Match 99.6%; Score 1363.2; DB 13; Length 2062;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1365; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 ATGGCCCTCTCCACCGTGCCTGACCTGCTGCTGCACCTGGTGTCTCTGAGCTGTGGTG 60

155 ATGGCCCTCTCCACCGTGCCTGACCTGCTGCTGCACCTGGTGTCTCTGAGCTGTGGTG 214

61 GGAATATATACCCCTCAGGGGTATTGGAGTGGTCCCTACCTAGGGGACAGGAGAGA 120

215 GGAATATATACCCCTCAGGGGTATTGGAGTGGTCCCTACCTAGGGGACAGGAGAGA 274

121 GATAGTGTGTGCCCAAGGAAATATATCCACCTCAAAATAATTCGATTGTGTACC 180

275 GATAGTGTGTGCCCAAGGAAATATATCCACCTCAAAATAATTCGATTGTGTACC 334

181 AAGTCCACAAAGGAACTACTGTGACATGCTGCCAGCCCGGGGACGATACGGAC 240

335 AAGTCCACAAAGGAACTACTGTGACATGCTGCCAGCCCGGGGACGATACGGAC 394

241 TGCAGGGAGTGTGAGAGCGGCTCCCTACCGCTTCAGAAAACCACTCAGACACGCTC 300

395 TGCAGGGAGTGTGAGAGCGGCTCCCTACCGCTTCAGAAAACCACTCAGACACGCTC 454

301 AGCTGCTCCAAATGCCAAAGGAAATGGTCCAGTGGAGATCTCTTTCACAGTGGAC 360

455 AGCTGCTCCAAATGCCAAAGGAAATGGTCCAGTGGAGATCTCTTTCACAGTGGAC 514

361 CGGACACCGTGTGGTGTGAGGAGAACCACTACCGGCAATATTGGAGTGAACCTT 420

515 CGGACACCGTGTGGTGTGAGGAGAACCACTACCGGCAATATTGGAGTGAACCTT 574

421 TTCCAGTGTCTCAATTGTCAGCTCTGCTCAATGGACCGTGCACCTCTCTCCGACGAG 480

575 TTCCAGTGTCTCAATTGTCAGCTCTGCTCAATGGACCGTGCACCTCTCTCCGACGAG 634

481 AAACAGAACACCGTGTGGACCTGCCATGCACTAGGTTTCTTCTTAAGAGAAAACGAGTGTCTC 540

635 AAACAGAACACCGTGTGGACCTGCCATGCACTAGGTTTCTTCTTAAGAGAAAACGAGTGTCTC 694

541 TCCTGTAGTAACTGTGAAGAAAGCCTGGAGTGCACGAGTGTGGCTTACCCACAGATTGAG 600


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Db 695 TCCGTAGTAAGTAAAGCCCTGGAGTGCAGAGTTGTGCTACCCAGATTGAG 754
QY 601 AATGTTAAGGCACTGAGGACTCAGCACCAGAGTGTGTCCTGCTGCTATTTCTTT 660
Db 755 AATGTTAAGGCACTGAGGACTCAGCACCAGAGTGTGTCCTGCTGCTATTTCTTT 814
QY 661 GGTCTTTGCTTTTATCCCTCTCTCTCATGTTGTTAATGATATCGTACCAAGGTGGAG 720
Db 815 GGTCTTTGCTTTTATCCCTCTCTCTCATGTTGTTAATGATATCGTACCAAGGTGGAG 874
QY 721 TCAAGCTCTACTCCATCTTTGTGGAAATCGACACCTGAAAGAGGGGAGCTTGA 780
Db 875 TCAAGCTCTACTCCATCTTTGTGGAAATCGACACCTGAAAGAGGGGAGCTTGA 934
QY 781 GGAACCTACTAAGCCCTGCGCCCAACCCAAAGCTTCAGTCCCACTCCAGGCTTCACC 840
Db 935 GGAACCTACTAAGCCCTGCGCCCAACCCAAAGCTTCAGTCCCACTCCAGGCTTCACC 994
QY 841 CCCACCTGGGCTTCACTCCGTCGCCAGTTCACCTTCACCTCCAGTCCACCTATACC 900
Db 995 CCCACCTGGGCTTCACTCCGTCGCCAGTTCACCTTCACCTCCAGTCCACCTATACC 1054
QY 901 CCGGTGACTGCCCAACTTTGGGCTCCCGCAGAGGTGGCACCACCTATCAGGG 960
Db 1055 CCGGTGACTGCCCAACTTTGGGCTCCCGCAGAGGTGGCACCACCTATCAGGG 1114
QY 961 GGTGAGCCCATCTTGGCAGACCCCTGCGCTCCGACCCCATCCCAACCCCTTCAGAAG 1020
Db 1115 GGTGAGCCCATCTTGGCAGACCCCTGCGCTCCGACCCCATCCCAACCCCTTCAGAAG 1174
QY 1021 TGGGAGGACAGCCCAAGCCACAGAGCTTAGACACTGATGACCCCGAGCGTGTAC 1080
Db 1175 TGGGAGGACAGTCCCAAGCCACAGAGCTTAGACACTGATGACCCCGAGCGTGTAC 1234
QY 1081 GCGGTGGTGGAGACGTGCGCCGTTGCGTGGAGGAATTCGTGGCGGCTTAGGGCTG 1140
Db 1235 GCGGTGGTGGAGACGTGCGCCGTTGCGTGGAGGAATTCGTGGCGGCTTAGGGCTG 1294
QY 1141 AGCGACACAGATCGATCGGTGGAGCTGCAGAGCGGCTGCTGCGGAGCGGCA 1200
Db 1295 AGCGACACAGATCGATCGGTGGAGCTGCAGAGCGGCTGCTGCGGAGCGGCA 1354
QY 1201 TACAGATGCTGGGACCTGGAGGCGGCGCAGCGGCGGAGCGGAGCTGGAGCTG 1260
Db 1355 TACAGATGCTGGGACCTGGAGGCGGCGCAGCGGCGGAGCGGAGCTGGAGCTG 1414
QY 1261 CTGGGACGCTGCTCCGACATGGACCTGCTGGGCTGCTGGAGGACATCGAGGAGCG 1320
Db 1415 CTGGGACGCTGCTCCGACATGGACCTGCTGGGCTGCTGGAGGACATCGAGGAGCG 1474
QY 1321 CTTTGGGCGCGCGCCCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
Db 1475 CTTTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1522
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RESULT 15

AAQ12215
ID AAQ12215 standard; DNA; 2176 BP.

XX AC AAQ12215;

XX DT 12-SEP-1991 (first entry)

XX DE Type I TNF receptor.

XX KW Tumour Necrosis Factor; TNF; binding protein; TBP-I; ss.

XX OS Homo sapiens.

XX FH Key

XX FT terminator

XX FT Location/Qualifiers

XX FT 244..246

XX FT /*tag= a

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FT CDS /note= "in-frame termination codon"
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FT /product= type I TNF receptor
FT 256..318
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FT 319..1620
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FT 319..864
FT misc_rna
FT 319..864
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FT /note= "may be 2 codons shorter or a few codons longer"
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FT 583..627
FT /*tag= f
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FT 850..858
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FT 889..957
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FT /*tag= j
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FT 634..756
FT /*tag= k
FT /number= 3
FT 757..858
FT /*tag= l
FT /number= 4
FT 2145..2150
FT /*tag= m
FT polyA_signal
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FT 12-JUL-1990; 90IL-0095064.
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FT 13-DEC-1989; 89IL-0092697.
FT
FT (YEDA ) YEDA RES & DEV CO LTD.
FT
FT Wallach D, Nopar Y, Kemper O, Engelmann H, Brakebusch C;
FT Aderka D;
FT
FT WPI; 1991-186774/26.
FT P-PSDB; AARI2550.
FT
FT Recombinant tumour necrosis factor binding protein I - prepd. by
FT transfecting eukaryotic cells with vector contg. deoxyribonucleic
FT acid encoding human type I TNF receptor or soluble domain
FT
FT Disclosure; Fig 1(D); 30pp; English.
FT
FT The Tumour Necrosis Factor Binding Protein I is the soluble form of
FT type I TNF-receptor and constitutes a fragment of the cell surface
FT form of this receptor, corresp. to its extracellular domain.
FT there is no characteristic poly(A) addition signal near the 3' end
FT of the cDNA. The sequence ACTAAA (tag m) may serve as an
FT alternative to this signal, but with low efficiency.
FT See also AAQ12212-15.
FT
FT Sequence 2176 BP; 475 A; 644 C; 602 G; 455 T; 0 other;
FT
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| | | | | | | | | | |
|--|------|--|------|--|--|--|--|--|--|
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| Best Local Similarity 99.6%; Score 1363.2; DB 12; Length 2176; | | | | | | | | | |
| Matches 1365; Conservative 0; Mismatches 3; Indels 0; Gaps 0; | | | | | | | | | |
| QY | 1 | ATGGCCCTCTCACCGTGCCTGACTGCTGCTGCGACCTGGTGCCTCGAGCTGTGGTG | 60 | | | | | | |
| DB | 256 | ATGGCCCTCTCACCGTGCCTGACTGCTGCTGCGCTGGTGCCTCGAGCTGTGGTG | 315 | | | | | | |
| QY | 61 | GGAAATATACCCCTCAGGGGTTTATGGACTGTGCTCCCTCACCTAGGGGACAGGGAGAGAGA | 120 | | | | | | |
| DB | 316 | GGAAATATACCCCTCAGGGGTTTATGGACTGTGCTCCCTCACCTAGGGGACAGGGAGAGAGA | 375 | | | | | | |
| QY | 121 | GATAGTGTGTGCCCAAGGAAATATATCCACCCCTCAAATAATATGATTTGCTGTACC | 180 | | | | | | |
| DB | 376 | GATAGTGTGTGCCCAAGGAAATATATCCACCCCTCAAATAATATGATTTGCTGTACC | 435 | | | | | | |
| QY | 181 | AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCGGGCGAGATACGGAC | 240 | | | | | | |
| DB | 436 | AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCGGGCGAGATACGGAC | 495 | | | | | | |
| QY | 241 | TGCAGGGAGTGTGAGAGCGGCTCCTTTCACCGCTTCAGAAAAACCACTCAGACACTGCCCTC | 300 | | | | | | |
| DB | 496 | TGCAGGGAGTGTGAGAGCGGCTCCTTTCACCGCTTCAGAAAAACCACTCAGACACTGCCCTC | 555 | | | | | | |
| QY | 301 | AGCTGCTCCAAATGCCAAAGAAATGGGTGAGTGGAGATCTCTTTCACACAGTGGAC | 360 | | | | | | |
| DB | 556 | AGCTGCTCCAAATGCCAAAGAAATGGGTGAGTGGAGATCTCTTTCACACAGTGGAC | 615 | | | | | | |
| QY | 361 | CGGACACCGTGTGGCTGCAGGAAGAACAGTACCGGCATTTATGGAGTGAACACCTT | 420 | | | | | | |
| DB | 616 | CGGACACCGTGTGGCTGCAGGAAGAACAGTACCGGCATTTATGGAGTGAACACCTT | 675 | | | | | | |
| QY | 421 | TTCCAGTGCCTCAATTTGAGCCTCTGCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG | 480 | | | | | | |
| DB | 676 | TTCCAGTGCCTCAATTTGAGCCTCTGCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG | 735 | | | | | | |
| QY | 481 | AAACAGACACCGTGTGCACCTGCCATGCGACGTTTCTTCTAAGAGAAAACAGTGTGTC | 540 | | | | | | |
| DB | 736 | AAACAGACACCGTGTGCACCTGCCATGCGACGTTTCTTCTAAGAGAAAACAGTGTGTC | 795 | | | | | | |
| QY | 541 | TCCTGTAGTAACTGTAGAAAAGCCTGGAGTGCACGAAGTTGTGCTTACCCAGATTGAG | 600 | | | | | | |
| DB | 796 | TCCTGTAGTAACTGTAGAAAAGCCTGGAGTGCACGAAGTTGTGCTTACCCAGATTGAG | 855 | | | | | | |
| QY | 601 | AATGTTAAGGCACTGAGGACTCAGGCAACACAGTGTGTTGCCCTGGTCAATTTCTTT | 660 | | | | | | |
| DB | 856 | AATGTTAAGGCACTGAGGACTCAGGCAACACAGTGTGTTGCCCTGGTCAATTTCTTT | 915 | | | | | | |
| QY | 661 | GGTCTTTGGCTTTTATCCCTCTCTCTCATTTGGTTTAAATGATCGCTACCAACGGTGGAG | 720 | | | | | | |
| DB | 916 | GGTCTTTGGCTTTTATCCCTCTCTCTCATTTGGTTTAAATGATCGCTACCAACGGTGGAG | 975 | | | | | | |
| QY | 721 | TCCAAGCTCTACTCCATTTGTTGGGAAATCGACACCTGAAAGAGAGGGGAGCTTGA | 780 | | | | | | |
| DB | 976 | TCCAAGCTCTACTCCATTTGTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGA | 1035 | | | | | | |
| QY | 781 | GGAACTACTACTAAGCCCTCGGCCCAACCCAAAGCTTCAGTCCCACTCCAGGCTTCACC | 840 | | | | | | |
| DB | 1036 | GGAACTACTACTAAGCCCTCGGCCCAACCCAAAGCTTCAGTCCCACTCCAGGCTTCACC | 1095 | | | | | | |
| QY | 841 | CCCACCTTGGGCTTCAGTCCCGTGCAGTTCACCTTCACCTCCAGCTCCACCTATACC | 900 | | | | | | |
| DB | 1096 | CCCACCTTGGGCTTCAGTCCCGTGCAGTTCACCTTCACCTCCAGCTCCACCTATACC | 1155 | | | | | | |
| QY | 901 | CCCGGTGACTGTCCCAACTTTGGGCTCCCGCGAGAGGTGGCACCACTATCAGGGG | 960 | | | | | | |
| DB | 1156 | CCCGGTGACTGTCCCAACTTTGGGCTCCCGCGAGAGGTGGCACCACTATCAGGGG | 1215 | | | | | | |
| QY | 961 | GCTGACCCCACTCTTGGGACAGCCCTCGCTTCGACCCCAATCCCAACCCCTTCAGAG | 1020 | | | | | | |
| DB | 1216 | GCTGACCCCACTCTTGGGACAGCCCTCGCTTCGACCCCAATCCCAACCCCTTCAGAG | 1275 | | | | | | |
| QY | 1021 | TGGGAGGACACGCCCAACCCACAGAGCCTAGACACTGATGACCCCGGACCGCTGTAC | 1080 | | | | | | |

Search completed: June 8, 2003, 23:42:11
Job time : 348 secs

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| QY | 1081 | GCCGTGTGGAGAAACGTGCCCGCTTGGCTTGGAGGAATTCGTGCGCGCTAGGGCTG | 1140 |
| DB | 1336 | GCCGTGTGGAGAAACGTGCCCGCTTGGCTTGGAGGAATTCGTGCGCGCTAGGGCTG | 1395 |
| QY | 1141 | AGCGACCAAGATCGATCGGCTGGAGCTGCAGAACCGGGCGCTGCCTGCGGAGGCGCAA | 1200 |
| DB | 1396 | AGCGACCAAGATCGATCGGCTGGAGCTGCAGAACCGGGCGCTGCCTGCGGAGGCGCAA | 1455 |
| QY | 1201 | TACAGCATGCTGGGCACTGAGGCGGCGCACCGCGGCGCGAGGCGCACGCTGGAGCTG | 1260 |
| DB | 1456 | TACAGCATGCTGGGCACTGAGGCGGCGCACCGCGGCGCGAGGCGCACGCTGGAGCTG | 1515 |
| QY | 1261 | CTGGGACGCTGCTCCGCGACATGACCTGCTGGGCTGCTGCGGAGGACATCGAGGCGG | 1320 |
| DB | 1516 | CTGGGACGCTGCTCCGCGACATGACCTGCTGGGCTGCTGCGGAGGACATCGAGGCGG | 1575 |
| QY | 1321 | CTTTGCGGCGCGCGCGCGCTCCCGCGCGCGCGCTTCTCTCAGATGA | 1368 |
| DB | 1576 | CTTTGCGGCGCGCGCGCGCTCCCGCGCGCGCGCTTCTCTCAGATGA | 1623 |

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2003, 22:32:19 ; Search time 3520 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1368 | 100.0 | 2112 | 9 | HUMTNFRP | M63121 Human tumor |
| 3 | 1368 | 100.0 | 2194 | 9 | BC010140 | BC010140 Homo sapi |
| 4 | 1366.4 | 99.9 | 2087 | 9 | HUMTNFR | M33294 Human tumor |
| 5 | 1366.4 | 98.9 | 2111 | 6 | A26412 | A26412 cDNA for (5 |
| 6 | 1366.4 | 99.9 | 2111 | 6 | AX409713 | AX409713 Sequence |
| 7 | 1366.4 | 99.9 | 2111 | 9 | HUMTNFRB | M58286 Homo sapien |
| 8 | 1366.4 | 99.9 | 2161 | 6 | AR096330 | AR096330 Sequence |
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| 11 | 1366.4 | 98.9 | 2175 | 6 | A78738 | A78738 Sequence 7 |
| 12 | 1366.4 | 99.9 | 2175 | 6 | AR041076 | AR041076 Sequence |
| 13 | 1366.4 | 99.9 | 2175 | 6 | I64751 | I64751 Sequence 1 |
| 14 | 1366.4 | 99.9 | 2176 | 6 | A19907 | A19907 Synthetic n |
| 15 | 1363.2 | 99.6 | 2062 | 6 | A21522 | A21522 TNF alpha q |
| 16 | 1360 | 99.4 | 2062 | 6 | I43805 | I43805 Sequence 24 |
| 17 | 1351.2 | 98.8 | 2061 | 6 | A20255 | A20255 55KD recept |
| 18 | 1344.4 | 98.3 | 2109 | 9 | AK056611 | AK056611 Homo sapi |
| 19 | 1323.2 | 96.7 | 2050 | 9 | HUMTNFRP | M60275 Human tumor |
| 20 | 1106 | 80.8 | 1331 | 6 | A29103 | A29103 H.sapiens m |
| 21 | 890.6 | 65.1 | 2171 | 4 | AB051103 | AB051103 Felis cat |
| 22 | 861 | 62.9 | 2004 | 4 | SSU19994 | U19994 Sus scrofa |
| 23 | 743.4 | 54.3 | 2115 | 10 | AF329976 | AF329976 Rattus no |
| 24 | 743.4 | 54.3 | 2115 | 10 | AF329977 | AF329977 Rattus no |
| 25 | 743.4 | 54.3 | 2130 | 6 | AX401925 | AX401925 Sequence |
| 26 | 743.4 | 54.3 | 2130 | 10 | RATTNFR | M63122 Rat tumor n |
| 27 | 741.8 | 54.2 | 2115 | 10 | AF329978 | AF329978 Rattus no |
| 28 | 741.8 | 54.2 | 2115 | 10 | AF329979 | AF329979 Rattus no |
| 29 | 741.8 | 54.2 | 2115 | 10 | AF329980 | AF329980 Rattus no |
| 30 | 741.8 | 54.2 | 2115 | 10 | AF329981 | AF329981 Rattus no |
| 31 | 690.4 | 50.5 | 1956 | 10 | MUSTNFR2 | M59377 Murine tumor |
| 32 | 690.4 | 50.5 | 2048 | 10 | MUSTNFR1 | M60468 Mouse tumor |
| 33 | 690.4 | 50.5 | 2063 | 10 | MMP55R | X59238 Murine mRNa |
| 34 | 690.4 | 50.5 | 2086 | 10 | BC004599 | BC004599 Mus muscu |
| 35 | 690.4 | 50.5 | 2154 | 10 | MUSTNFX | L26349 Mus musculu |
| 36 | 690.4 | 50.5 | 2179 | 10 | MMTNFRS | X57796 Mouse mRNa |
| 37 | 685.4 | 50.1 | 2440 | 4 | BTU90937 | U90937 Bos taurus |
| 38 | 632.8 | 46.3 | 6896 | 6 | AR031375 | AR031375 Sequence |
| 39 | 632.8 | 46.3 | 6896 | 6 | BD009743 | BD009743 Compositi |
| 40 | 632.4 | 46.2 | 6889 | 6 | I26928 | I26928 Sequence 2 |
| 41 | 596.8 | 43.6 | 600 | 6 | A20257 | A20257 Synthetic n |
| 42 | 593.6 | 43.4 | 600 | 6 | I43808 | I43808 Sequence 47 |
| 43 | 514 | 37.6 | 1301 | 6 | AR131310 | AR131310 Sequence |
| 44 | 514 | 37.6 | 1301 | 6 | AR134762 | AR134762 Sequence |
| 45 | 510 | 37.3 | 510 | 6 | A21525 | A21525 oligonucleo |

ALIGNMENTS

RESULT 1

| | | | | | |
|------------|---|------------|-----|--------|-----------------|
| RESULT 1 | A29098 | 1368 bp | DNA | linear | PAT 03-JUL-1995 |
| LOCUS | A29098 | | | | |
| DEFINITION | Synthetic DNA for TNF-receptor from patent EP0393438. | | | | |
| ACCESSION | A29098 | | | | |
| VERSION | A29098.1 | GI:1248892 | | | |
| KEYWORDS | synthetic construct. | | | | |
| SOURCE | synthetic construct | | | | |
| ORGANISM | artificial sequences. | | | | |
| REFERENCE | 1 (bases 1 to 1368) | | | | |
| AUTHORS | Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,C. | | | | |
| TITLE | TNF-receptor, TNF-binding protein and DNA coding therefor | | | | |
| JOURNAL | Patent: EP 0393438-A 48 24-OCT-1990; | | | | |
| | BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H | | | | |

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FEATURES             Location/Qualifiers
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     /organism="synthetic construct"
     /db_xref="taxon:32630"
BASE COUNT          293 a 424 c 375 g 276 t
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Query Match          100.0%; Score 1368; DB 6; Length 1368;
Best Local Similarity 100.0%; Pred. No. 1e-265;
Matches 1368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGGCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCTCTGGAGCTTTGGTG 60
Db 1 ATGGGGCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCTCTGGAGCTTTGGTG 60
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Db 61 GGAATATACCCCTCAGGGGTTATTGGAGTGTGCTCCTCACCCTAGGGGACAGGGAAGAGA 120
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Db 121 GATAGTGTGTCCCAAGGAAATATATACACCTCAAAATAATTCGATTGTGTACC 180
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RESULT 2
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LOCUS             Human tumor necrosis factor receptor (TNF receptor) mRNA, complete
DEFINITION        cds.
ACCESSION         M3121 M75861
VERSION           M3121.1 GI:339755
KEYWORDS          tumor necrosis factor receptor.
SOURCE            Human cDNA to mRNA.
ORGANISM          Homo sapiens
REFERENCE         1 (bases 1 to 2112)
AUTHORS           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                  Himmeler A., Maurer-Fogy I., Kronke M., Scheurich P.,
                  Pfizenmaier K., Lantzi M., Olsson I., Hauptmann R., Stratowa C. and
                  Adolf G.R.
TITLE             Molecular cloning and expression of human and rat tumor necrosis
                  factor receptor chain (p80) and its soluble derivative, tumor
                  necrosis factor-binding protein
JOURNAL           DNA Cell Biol. 9 (10), 705-715 (1990)
MEDLINE          91090841
PUBMED           1702293
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[illegible]


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Db 796 TCCTGTAGTAACTGTAAAGAAAGCCTGGAGTGCAGAAAGTTGTCTTCTTCTTCTTCTTCTT 855
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Db 916 GTCCTTTTCCCTTTATCCCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 975
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DEFINITION Sequence 1 from Patent EP0657536.
ACCESSION A43873
VERSION A43873.1 GI:2299022
KEYWORDS
SOURCE unidentified.
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ORGANISM unidentified
REFERENCE 1 (bases 1 to 2175)
AUTHORS Wallach,D., Brackebusch,C., Varfolomeev,B. and Batkin,M.
TITLE proteases capable of shedding the soluble TNF-receptor and TNF-R
derived peptides and antibodies against the proteases inhibiting
the shedding
Patent: EP 0657536-A 1 14-JUN-1995;
JOURNAL YEDA RES & DEV (IL)
COMMENT Other publication ZA 9407962 951121
Other publication JP 7194376 950801
Other publication AU 7574294 950504
Other publication CA 2133872 950413.
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BASE COUNT 474 a 641 c 604 g 456 t
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Query Match 99.9%; Score 1366.4; DB 6; Length 2175;
Best Local Similarity 99.9%; Pred. No. 2.1e-265;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 616 CGGACACCGTGTGCTGCGTGCAGGAAGAACAGTACCGGCGATTAATTTGAGTGAACACCTT 675
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RESULT 12
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LOCUS Sequence 1 from patent US 5811261.
DEFINITION AR041076
ACCESSION AR041076
VERSION AR041076.1 GI:5961572
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2175)
AUTHORS Wallach,D., Nophar,Y., Kemper,O., Engelmann,H., Brakebusch,C. and Aderka,D.
TITLE Expression of the recombinant tumor necrosis factor binding protein I (TBP-I)
JOURNAL Patent: US 5811261-A 1 22-SEP-1998;
FEATURES Location/Qualifiers
source 1..2175
BASE COUNT 474 a 641 c 604 g 456 t
ORIGIN

Query Match 99.9%; Score 1366.4; DB 6; Length 2175;
Best Local Similarity 99.9%; Pred. No. 2.1e-265;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGGCGCTCTCACCGTGGCTGACCTGCTGCTGCGCACTGGTGTCTCTGGAGCTGTGGTG 60
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| Query Match | 99.9% | Score 1366.4 | DB 6 | Length 2176 |
| Best Local Similarity | 99.9% | Pred. No. 2.1e-265 | | |
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| QY | 61 | GGAAATATACCCCTCAGGGGTTATTGGACTTGGTCCCTCACCCTAGGGGACAGGGAGAAGAAGA | 120 |
| DB | 316 | GGAAATATACCCCTCAGGGGTTATTGGACTTGGTCCCTCACCCTAGGGGACAGGGAGAAGAAGA | 375 |
| QY | 121 | GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAAAATAATTCGATTGTGTGTAAC | 180 |
| DB | 376 | GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAAAATAATTCGATTGTGTGTAAC | 435 |
| QY | 181 | AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGAC | 240 |
| DB | 436 | AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGAC | 495 |
| QY | 241 | TGCAGGAGTGTGAGACGGCTCCTTCCACCGCTTCAGAAAAACACCTCAGACACTGGCTC | 300 |
| DB | 496 | TGCAGGAGTGTGAGACGGCTCCTTCCACCGCTTCAGAAAAACACCTCAGACACTGGCTC | 555 |
| QY | 301 | AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAAGTGGAGATCTCTTTTGCACAGTGGAC | 360 |
| DB | 556 | AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAAGTGGAGATCTCTTTTGCACAGTGGAC | 615 |
| QY | 361 | CGGGACACCGTGTGTGCTCGAGGAACACCAAGTACCGGCATATTGGAGTGAACACTT | 420 |
| DB | 616 | CGGGACACCGTGTGTGCTCGAGGAACACCAAGTACCGGCATATTGGAGTGAACACTT | 675 |
| QY | 421 | TTCCAGTGTCTCAATTTCAGCCTCTGCTCAATGGGACCGTGCACCTCTCTGCGCAGGAG | 480 |
| DB | 676 | TTCCAGTGTCTCAATTTCAGCCTCTGCTCAATGGGACCGTGCACCTCTCTGCGCAGGAG | 735 |
| QY | 481 | AAACAGAACACCGTGTGCTGACCTGCCATGCAAGTTTCTTCTAAGAGAAAAACGAGTGTGTC | 540 |
| DB | 736 | AAACAGAACACCGTGTGCTGACCTGCCATGCAAGTTTCTTCTAAGAGAAAAACGAGTGTGTC | 795 |
| QY | 541 | TCCTGTAGTAACTGTAGAAAAAGCCTGGAGTGCACGAAGTTGTGCTTACCCAGATTGAG | 600 |
| DB | 796 | TCCTGTAGTAACTGTAGAAAAAGCCTGGAGTGCACGAAGTTGTGCTTACCCAGATTGAG | 855 |
| QY | 601 | AATGTTAAGGCACTGAGGACTCAGGACACACAGTGTGTTGCCCTGGTCAATTTCTCTT | 660 |
| DB | 856 | AATGTTAAGGCACTGAGGACTCAGGACACACAGTGTGTTGCCCTGGTCAATTTCTCTT | 915 |
| QY | 661 | GGTCTTTGGCCTTTATCCCTCCCTCTCAATTGGTTTAATGATACGCTACCAACGTTGAAG | 720 |
| DB | 916 | GGTCTTTGGCCTTTATCCCTCCCTCTCAATTGGTTTAATGATACGCTACCAACGTTGAAG | 975 |
| QY | 721 | TCCAAGCTCTACTCCATTTGTTGGGAAATCGACACCTGANAAGAGGGGGAGCTTGAA | 780 |
| DB | 976 | TCCAAGCTCTACTCCATTTGTTGGGAAATCGACACCTGANAAGAGGGGGAGCTTGAA | 1035 |
| QY | 781 | GGAACTACTACTAAGCCCTCGGCCCAACCCAAAGCTTCAGTCCCACTCCAGGCTTCACC | 840 |
| DB | 1036 | GGAACTACTACTAAGCCCTCGGCCCAACCCAAAGCTTCAGTCCCACTCCAGGCTTCACC | 1095 |
| QY | 841 | CCCACCTGGGCTTACGTCGCTGCCAGTTCCACCTTCACTCCAGCTCCACCTATACC | 900 |
| DB | 1096 | CCCACCTGGGCTTACGTCGCTGCCAGTTCCACCTTCACTCCAGCTCCACCTATACC | 1155 |
| QY | 901 | CCGGGTGACTGTCCCAACTTTGGGGCTCCCGGACAGAGGTGGACACCACTATCAGGG | 960 |
| DB | 1156 | CCGGGTGACTGTCCCAACTTTGGGGCTCCCGGACAGAGGTGGACACCACTATCAGGG | 1215 |
| QY | 961 | GCTGACCCCATCTTTGGACAGCCCTCGCTCTCGGACCCCATCCCAACCCCTTCAGAAG | 1020 |
| DB | 1216 | GCTGACCCCATCTTTGGACAGCCCTCGCTCTCGGACCCCATCCCAACCCCTTCAGAAG | 1275 |
| QY | 1021 | TGGGAGGACAGCGCCCAAGCCACAGAGCTTAGACACTGATGACCCCGGAGCGCTGAC | 1080 |

[illegible]

Db 275 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCTCAAAATATTCGATTTGCTGTACC 334
QY 181 AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCGCGGGGAGGATACGGAC 240
Db 335 AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCGCGGGGAGGATACGGAC 394
QY 241 TGCAGGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAACCACTCAGACACATGCCCTC 300
Db 395 TGCAGGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAACCACTCAGACACATGCCCTC 454
QY 301 AGCTGCTCCAAATGCCAAAGGAAATGGGTGAGGTGAGATCTCTTTGACAGTGGAC 360
Db 455 AGCTGCTCCAAATGCCAAAGGAAATGGGTGAGGTGAGATCTCTTTGACAGTGGAC 514
QY 361 CGGGACACCGTGTGTGGCTGAGGAGAACACAGTACCGGCATTTATGGAGTGAACACCTT 420
Db 515 CGGGACACCGTGTGTGGCTGAGGAGAACACAGTACCGGCATTTATGGAGTGAACACCTT 574
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Db 575 TTCCAGTGTCTCAATTTGACGCTCTGCTCAATGGAGCGTGCACCTCTCCTGCCAGGAG 634
QY 481 AAACAGACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGC 540
Db 635 AAACAGACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGC 594
QY 541 TCCTGTAGTAAGTGAAGAAAGCCTGGAGTGCACGAAATTTGTGCTACCCAGATTTGAG 600
Db 695 TCCTGTAGTAAGTGAAGAAAGCCTGGAGTGCACGAAATTTGTGCTACCCAGATTTGAG 754
QY 601 AATGTTAAGGACACTGAGGACACTCAGGCACACAGTGTGCTGCTGCTGCTGCTGCTT 560
Db 755 AATGTTAAGGACACTGAGGACACTCAGGCACACAGTGTGCTGCTGCTGCTGCTGCTT 814
QY 661 GCTCTTTGCTTTTATCCCTCTCTTCAATTTGTTTAAATGATGCTTACCAACGGTGAAG 720
Db 815 GCTCTTTGCTTTTATCCCTCTCTTCAATTTGTTTAAATGATGCTTACCAACGGTGAAG 874
QY 721 TCCAGCTCTACTCCATTTGTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGAA 780
Db 875 TCCAGCTCTACTCCATTTGTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGAA 934
QY 781 GGAAGTACTACTAAGCCCTGCGCCCAACCAAGCTTCAGTCCCACTCCAGGCTTCACC 840
Db 935 GGAAGTACTACTAAGCCCTGCGCCCAACCAAGCTTCAGTCCCACTCCAGGCTTCACC 994
QY 841 CCCAGCTGGGCTTCAGTCCCTGCGCCAGTTCACCTTCACCTCCAGCTCCACCTATACC 900
Db 995 CCCAGCTGGGCTTCAGTCCCTGCGCCAGTTCACCTTCACCTCCAGCTCCACCTATACC 1054
QY 901 CCCGTTGACTGTCCCAACTTTGCGGCTCCCGCAGAGAGTGGCACCCCTATCAGGGG 960
Db 1055 CCCGTTGACTGTCCCAACTTTGCGGCTCCCGCAGAGAGTGGCACCCCTATCAGGGG 1114
QY 961 GCTGACCCCATCTTGCAGACGCTTCGCTCCGACCCCATCCCAACCCCTTCAGAG 1020
Db 1115 GCTGACCCCATCTTGCAGACGCTTCGCTCCGACCCCATCCCAACCCCTTCAGAG 1174
QY 1021 TGGGAGGACAGCGCCACAAAGCCACAGAGCTAGACACTGATGACCCCGCGAGCTGTAC 1080
Db 1175 TGGGAGGACAGTGCACAAAGCCACAGAGCTAGACACTGATGACCCCGCGAGCTGTAC 1234
QY 1081 GCCGTGGTGAAGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
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Db 1295 ACGGACACAGATCGATCGGCTGGAGCTGCAGAGCGGCGCTGCTGCTGCTGCTGCTG 1354
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QY 1261 CTGGGACGGGTGCTCCGCGACATGGACCTGCTGGGGTGGCTGGAGACATCGAGGAGCG 1320
Db 1415 CTGGGACGGGTGCTCCGCGACATGGACCTGCTGGGGTGGCTGGAGACATCGAGGAGCG 1474
QY 1321 CTTTGGGGCCCGCGCCGCTCCCGCCGCGCGCCAGTCTTCTCAGATGA 1368
Db 1475 CTTTGGGGCCCGCGCCGCTCCCGCCGCGCGCCAGTCTTCTCAGATGA 1522

Search completed: June 9, 2003, 01:12:25
Job time : 3526 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2003, 01:12:29 ; Search time 1566 Seconds
(without alignments)
4705.585 Million cell updates/sec

Title: US-09-899-422A-2

Perfect score: 2487

Sequence: 1 MGLSTVPDLLPLVLELLV.....DIEEALCGPALPPAPSLLR 455

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DEV=slp
-Q/cgn2_1/USPTO.spool/US09899422/runat_04062003_145737_14712/app_query.fasta_1.647
-DB=EST -OPMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR=SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09899422.ecgn_1_1_2874 @runat_04062003_145737_14712 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPOP=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_ptc:*
- 27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1536 | 61.8 | 931 | 14 | BQ723672 |
| 2 | 1416 | 56.9 | 957 | 9 | AL559050 |
| 3 | 1416 | 56.9 | 1076 | 14 | BM923204 |
| 4 | 1292 | 52.0 | 741 | 13 | BI860918 |
| 5 | 1271.5 | 51.1 | 1070 | 13 | BM546826 |
| 6 | 1268 | 51.0 | 761 | 9 | AU131978 |
| 7 | 1261 | 50.7 | 942 | 9 | AL529836 |
| 8 | 1245.5 | 50.1 | 975 | 9 | AL577008 |
| 9 | 1234 | 49.6 | 974 | 12 | BI80101 |
| 10 | 1211.5 | 48.7 | 984 | 14 | BM800044 |
| 11 | 1206 | 48.5 | 889 | 9 | AU117362 |
| 12 | 1202 | 48.3 | 916 | 13 | BI757305 |
| 13 | 1195.5 | 48.1 | 718 | 12 | BI806079 |
| 14 | 1194 | 48.0 | 669 | 14 | BM742388 |
| 15 | 1191 | 47.9 | 837 | 9 | AL522989 |
| 16 | 1167 | 46.9 | 696 | 14 | BM899994 |
| 17 | 1152 | 46.3 | 818 | 13 | BI821169 |
| 18 | 1149.5 | 46.2 | 969 | 12 | BE871809 |
| 19 | 1126.5 | 45.3 | 859 | 13 | BI870917 |
| 20 | 1113 | 44.8 | 636 | 12 | BI803257 |
| 21 | 1113 | 44.8 | 1131 | 13 | BM467058 |
| 22 | 1110.5 | 44.7 | 761 | 12 | BI828278 |
| 23 | 1108.5 | 44.6 | 769 | 9 | AL522226 |
| 24 | 1096.5 | 44.1 | 872 | 13 | BI769006 |
| 25 | 1074 | 43.2 | 643 | 12 | BI8680356 |
| 26 | 1071.5 | 43.1 | 602 | 14 | BM791206 |
| 27 | 1070.5 | 43.0 | 627 | 14 | BM763879 |
| 28 | 1063.5 | 42.8 | 845 | 9 | AU125021 |
| 29 | 1056 | 42.5 | 575 | 14 | BM705174 |
| 30 | 1055 | 42.4 | 872 | 14 | BI723589 |
| 31 | 1052 | 42.3 | 1008 | 14 | BI719773 |
| 32 | 1048 | 42.1 | 859 | 9 | AU124446 |
| 33 | 1046 | 42.1 | 767 | 9 | AU142156 |
| 34 | 1037 | 41.7 | 576 | 12 | BM820201 |
| 35 | 1037 | 41.7 | 936 | 12 | BM81438 |
| 36 | 1034.5 | 41.6 | 971 | 12 | BE876920 |
| 37 | 1028 | 41.3 | 811 | 12 | BF342334 |
| 38 | 1017 | 40.9 | 772 | 9 | AU137990 |
| 39 | 1015.5 | 40.8 | 823 | 13 | BI766980 |
| 40 | 1010.5 | 40.6 | 929 | 12 | BI677121 |
| 41 | 1004 | 40.4 | 951 | 14 | BI882704 |
| 42 | 996.5 | 40.1 | 915 | 14 | BI881180 |
| 43 | 995.5 | 40.0 | 739 | 13 | BI520191 |
| 44 | 991 | 39.8 | 913 | 14 | BI926409 |
| 45 | 985 | 39.6 | 817 | 9 | AU125680 |

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION BQ723672
clone IMAGE:6184295 5', mRNA sequence.
ACCESSION BQ723672
VERSION BQ723672.1 GI:21862569
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 931)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)

BQ723672 931 bp mRNA linear EST 16-JUL-2002
AGENCOURT_8489850 Lupski_dorsal_root_ganglion Homo sapiens CDNA

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9pbbs-re@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13573 row: d column: 24
High quality sequence stop: 607.
Location/Qualifiers
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/db_xref="taxon:9606"
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/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TGAACCCACGGCTCCG-3' and
5'-GACTAGTTCAGATCGGAGCGGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

FEATURES
source

BASE COUNT 218 a 283 c 224 g 204 t 2 others
ORIGIN

Alignment Scores:

Pred. No.: 3 85e-137 Length: 931
Score: 1536.00 Matches: 289
Percent Similarity: 94.4% Conservative: 2
Best Local Similarity: 93.83% Mismatches: 10
Query Match: 61.76% Indels: 7
DB: 14 Gaps: 4

US-09-899-422a-2 (1-455) x B0723672 (1-931)

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Db 62 TGCTGTACCAAGTCCCAAGAGAACCTTACTGTACAAATGACTGTCCAGGCCGGGGCAG 121
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QY 98 HisCysLeuSerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCys 117
Db 182 CACTGCCTCAGCTGCTCAATGCGGAAGGAATGGTCCAGTGGAGATCTCTCTTTCG 241
QY 118 ThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSer 137
Db 242 ACAGTGGACGGGACACCGTGTGGCTGCAGGAAGAACACAGTACCGGCATTATTGGAGT 301
QY 138 GluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSer 157
Db 302 GAAACCTTTTCCAGTCTTCAATGACGCTCTGCCCTCAATGGGACCGTCACCTCTCC 361
QY 158 CysGlnGluLysGlnAsnThrValCysThrCysHisAlaGlyPheLeuArgGluAsn 177
Db 362 TGCCAGGAGAAACAGACCGGTGTGCACCTGCCATGCGAGGTTCTTCTTCTAGAGAAAC 421

QY 178 GluCysValSerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuPro 197
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QY 278 GlyPheThrProThrLeu-GlyPheSerProValProSerSerThrPheThrSerSer 297
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QY 334 Ile---ProAsnProLeu 338
Db 902 ATTCCCAACCCCTT 919
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LOCUS AL559050 LTI_NFL008_Tc2 Homo sapiens cDNA clone CS0DJ010YB05 5
DEFINITION prime, mRNA sequence.
ACCESSION AL559050
VERSION AL559050.1 GI:12904166
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 957)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Location/Qualifiers
1. .957
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/db_xref="taxon:9606"
/clone="CS0DJ010YB05"
/clone_lib="LTI_NFL008_Tc2"
/sex="male"
/tissue_type="T cells from T cell leukemia"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :

| | | | | | |
|------------|--------------------|-------------|--------------|------------|-----------------|
| BM923204 | BM923204 | 1076 bp | mRNA | linear | EST 12-MAR-2002 |
| LOCUS | ACENGCOURT_6625801 | NIH_MGC_116 | Homo sapiens | cdna clone | IMAGE:5758757 |
| DEFINITION | 5', mRNA sequence. | | | | |
| ACCESSION | BM923204 | | | | |
| VERSION | BM923204.1 | GI:19373583 | | | |

Db 314 TTCAGTCCGTCGCGAGTCCACCTTACCTCCAGCTCCACCTATACCCCCGGGTGACGT 373

Qy 305 ProAsnPhaAlaAlaProArgArgGluValAlaProProTyroGlnGlnValAlaAspProfile 324

Db 374 CCCAACTTTGGCGTCCCGCAGAGAGGTGCGACACCTATCAGGGGCTGACCCCATC 433

Qy 325 LeuAlaThrAlaLeuAlaSerAspProfileProAsnProLeuGlnLysTrpGluAspSer 344

Db 434 CTTGGCAGAGCCCTCGCTCCGAGCCCATCCCAACCCCTTCAGAACTGGGAGGACAGC 493

Qy 345 AlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyroAlaValValGlu 364

Db 494 GCCCACAAGCCACAGAGCCTAGACACTGATACCCCGCAGCCTGTACCCGCTGGTGAG 553

Qy 365 AsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeuSerAspHisGlu 384

Db 554 AACGTGCCCGCTGGCGTGAAGGAATTCGTGCGGCGCTAGGCTGAGGACACACAG 613

Qy 385 IleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGlnTyroSerMetLeu 404

Db 614 ATCGACTGGCTGGAGCTGCAGAACGGGCTGCCCTGGCGAGGCGCATACAGCATGCTG 673

Qy 405 AlaThrTyrArgArgArgThrProArgArgGluAlaThrLeuGluLeuGlyArgVal 424

Db 674 CGACCTGGAGCGGCGGCACCCCGCGCGGAGCCAGCTGGAGCTCTGGAGCGCGTG 733

Qy 425 LeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAlaLeuCysGlyPro 444

Db 734 CTCGCGACATGGACCTCTGGCTGGCTGGGAGCATCGAGGANGCGCTTGGGCCCC 793

Qy 445 AlaAlaLeuProProAlaProSerLeuLeuArg 455

Db 794 GNCGCCCTTCGCGCGCGCCAGCTTCTCAGA 826

RESULT 4

BI860918 741 bp mRNA linear EST 10-OCT-2001

LOCUS 603390284F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5399108 5',

DEFINITION mRNA sequence.

BI860918

BI860918.1 GI:16001653

EST.

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 741)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/BTP

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

plate: L1A112017 row: h column: 21

High quality sequence stop: 740.

Location/Qualifiers

1..741

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5399108"

/tissue_type="mammary adenocarcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 1.383 kb. Library enriched for

full-length clones and constructed by Life Technologies.

BASE COUNT 167 a Note: this is a NIH_MGC Library."

ORIGIN 229 c 175 g 170 t

Alignment Scores:

Pred. No.: 7,89e-114 Length: 741

Score: 1292.00 Matches: 241

Percent Similarity: 98.78% Conservative: 1

Best Local Similarity: 98.37% Mismatches: 2

Query Match: 51.95% Indels: 2

DB: 13 Gaps: 0

US-09-899-422a-2 (1-455) x BI860918 (1-741)

Qy 87 GlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeuSerCysSerLysCysArg 106

Db 3 GGCTCCTTCACCGCTTCAGAAACACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGA 62

Qy 107 LysGluMetGlyGlnValGluIleSerSerCysThrValAspArgAspThrValCysGly 126

Db 63 AAGAAATGGGTGAGTGGAGATCTCTTTCACAGTGGACCGGACACCGTGTGTGGC 122

Qy 127 CysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeuPheGlnCysPheAsnCys 146

Db 123 TGCAGGAAGAACCACTACCGCATTTATGGAGTGAACACCTTTTCCAGTGTCTCAATTCG 182

Qy 147 SerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCys 166

Db 183 AGCTCTGCTCATGGGACCGTGCACCTCTCTCCAGGAGAAACAGAACACCGTGTGC 242

Qy 167 ThrCysHisAlaGlyPheLeuArgGluAsnGluCysValSerCysSerAsnCysLys 186

Db 243 ACCTGCCATGCAGGTTCTTTTAAGAGAAACAGTGTCTCTCTGTAGTAACCTGTAAAG 302

Qy 187 LysSerLeuGluCysThrLysLeuCysLeuProGlnIleGluAsnValLysGlyThrGlu 206

Db 303 AAAAGCTGGAGTGCAGCAAGTTGTGCTACCCAGATTTGAGAATGTTAAGGGCACTGAG 362

Qy 207 AspSerGlyThrThrValLeuProLeuValIlePhePheGlyLeuCysLeuSer 226

Db 363 GACTCAGGCACCAAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422

Qy 227 LeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLysSerLysLeuTyrSerIle 246

Db 423 CTCCTCTCATTTGTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 482

Qy 247 ValCysGlyLysSerThrProGluLysGluGlyGluLeuGlyThrThrThrLysPro 266

Db 483 GTTTGTGGGAATGCACACCTGAAAAGAGGGGGAGCTTGAAGGAACCTACTACTAAGCC 542

Qy 267 LeuAlaProAsnProSerPheSerProThrProGlyPheThrProThrLeuGlyPheSer 286

Db 543 CTGCCCCCAACCAAGCTTCAGTCCACCTCCAGCTTCACCCCACTCCGGGCTTCAGT 602

Qy 287 ProValProSerSerThrPheThrSerSerSerThrThrThrProGlyAspCysProAsn 306

Db 603 CCCGTGCCAGTTCACCTTCACCTCCAGCTCCACCTATACCCCGGTGACTGTCCCAAC 662

Qy 307 PheAlaAlaProArgGluValAlaProProTyrGln-GlyAlaAspProIleLeuAl 326

Db 563 TTTCCGGCTCCCGC-AGAGAGGTGGCACCCCTATCAGGGGGGCTGACCCCTCTTCG 721

Qy 326 aThrAlaLeuAla 330

Db 722 GACAAGCTCGCT 734

RESULT 5

BI860918

LOCUS

DEFINITION

5', mRNA sequence.

ACCSSION

VERSION

BI860918 1070 bp mRNA linear EST 20-FEB-2002

AGENCOURT 6491128 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:573557

BI860918

BI860918.1 GI:18780096


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Db      654 TTCCAGTGTCTCAATTGACGCTCTGCCCTCAATGGGACCGTGCACCTCTCCCTGCCAGGAG 713
QY      161 LysGlnAsnThrValCysThrCysHisAlaGly-PhePheLeuArgGluAsnGluCysVa 180
Db      714 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTCCTTTTCAAGAGAAACGAGGTGT 773
QY      180 lSerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleG1 200
Db      774 CTCCTGTACTAGTGTAAAGADAAGCCTGGAGTGCACGAG-TTGTGCTACCCAGATTGA 832
QY      200 uAsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePh 220
Db      833 GAATGTTAAGGCACTAGACACTCAGGCACACAGTGCCTGTCCTCCCTGCTCAATTTCTT 892
QY      220 eGlyLeuCysLeuSerLeuPheIleGlyLeuMetTyrArgTyr 236
Db      893 TGTCTGTGCTTTTATMCTCTCTCTTCATTTGTTTAAATGTATCGCTAC 941

RESULT 8
AL577008 975 bp mRNA linear EST 16-FEB-2001
LOCUS AL577008 LRI_NFL006.PL2 Homo sapiens cDNA clone CS0DI082YA01 5
DEFINITION prime, mRNA sequence.
ACCESSION AL577008
VERSION AL577008.1 GI:12939716
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 975)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. .975
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI082YA01"
/clone_lib="LRI_NFL006.PL2"
/tissue_type="placenta"
/notes="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 231 a 258 c 259 g 221 t 6 others
ORIGIN

Alignment Scores:
Pred. No.: 3 63e-109 Length: 975
Score: 1245.50 Matches: 232
Percent Similarity: 96.27% Conservative: 0
Best Local Similarity: 96.27% Mismatches: 8
Query Match: 50.08% Indels: 4
DB: 9 Gaps: 0

US-09-899-422a-2 (1-455) x AL577008 (1-975)

QY      1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuVal 20
Db      256 ATGGGCTCTCCACCGCTGCTGACCTGCTGCTGCCACTGCTGCTGCTGCTGCTGCTGCTG 315
QY      21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40

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Db      316 GGAATATACCCCTCAGGGGTATTGGACTGTGTCCTCACCTAGGGACAGGAGAGA 375
QY      41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
Db      376 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCCAAAATATTCGATTCTGTTACC 435
QY      61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
Db      436 AAGTGCACAAAGAAACCTTACTTGTACATGACTGTCCAGGCGCGGGCAGGATACGAC 495
QY      81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
Db      496 TGCAGGAGTGTGAGCGGCTCCTTCACCGCTTCAGAAACACCACTCAGACACTGCCTC 555
QY      101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
Db      556 AGCTGCTCCAAATGCCGAAGGAATGGTCAAGTGGAGATCTCTTCTCCACAGTGGAC 615
QY      121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
Db      616 CGGGACACCGTGTGTGCTGCAGGAAGAACCACTACCGGCATTATTGGAGTGAACCTT 675
QY      141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
Db      676 TTCACGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCTCTCCAGGAG 735
QY      161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
Db      735 AAACAGAACACCGTGTGCTGCCCTGCCATGCACTTCTTCTTAAGAGAAACAGAGTGTGTC 795
QY      181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeu-CysLeuProGlnIleG1 200
Db      796 TYCTGTAGTAACCTGTAGAAAAGCCTGGAGTGCACGAAGTTGTGCTACCCAGATTGA 855
QY      200 uAsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePh 220
Db      856 GAATGTTAAGGCACTGAGGACTCAGGCACCAAMAGTCTGTTGCCCTGTGCTATTCTT 915
QY      220 eGlyLeuCysLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
Db      916 TGCTCTTGTGCT-TTATCCCC-CTCTTCATGCTTTAATGATGCTGCTACCAAGS-TGGAA 972
QY      240 s 240
Db      973 G 973

RESULT 9
LOCUS BG180101
DEFINITION BG180101 Homo sapiens cDNA clone IMAGE:4431019 5',
mRNA sequence.
ACCESSION BG180101.1 GI:12686804
VERSION BG180101
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 974)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10185 row: g column: 20

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QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
DB 226 GGAATATACCCCTCAGGGTATTGGAGTGGTCCCTCAGTGGGACAGGAGAGAGA 285
QY 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAspSerIleCysCysThr 60
DB 286 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 345
QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
DB 346 AAGTCCCAACAAGGAACCTACTGTGTACAAATGACTCTCCAGGCGCGGCGAGGATACGGAC 405
QY 81 CysArgGluCysLysSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
DB 406 TCCAGGGAGTGTGAGAGGGCTCTTCACCGCTTCAGAAACCACTCAGACACTGCCCTC 465
QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
DB 466 AGCTGCTCCAAATGCCGAAGAAATGGTCAAGTGGAGATCTCTTCTGGCACAGTGGAC 525
QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
DB 526 CGGGACACCGTGTGTGGTGCAGGAAGAACCACTACAGCATTTATTGGAGTGAACACCTT 585
QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
DB 586 TTCAGTGTCTCAATGGAGCCTCTGCCTCAATGGAGCGTGCACCTCTCCTGCCAGGAG 645
QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
DB 646 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTCTTCTTAAGAGAAACAGGTGTCTC 705
QY 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGln-IleG1 200
DB 706 TCCTGTAGTAAGTGAAGAAAGCCTGGAGTGCAGCAAGTGTGCTACCCACCATGNA 765
QY 200 uasnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIle-Phe- 219
DB 766 GAATGTTAAGGCACTGGAGCTCAGGACCACTGCTGTGTGTGCTGCTGCTGCTGCTGCT 825
QY 220 PheGlyLeuCysLeuSerLeu---LeuPheIleGlyLeuMetTyrArgTyrGlnArg 238
DB 826 TTTGGCTGCTCCTTTATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 885
QY 239 ---TrpLysSerLysLeuTyr-SerIleValCys-GlyLysSerThrPro-----GluL 255
DB 886 GGGGAAATCCAAAGCTCTACCTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 945
QY 255 ysGluGlyGluLeuGluGlyThrThrThrLysProLeuAlaProAsnProSerPheSerP 275
DB 946 AAGAAGGG-----GGGAAACCTTTGTG-AAGGAACCTTCC---TCCTC 983
QY 275 roThPro 277
DB 984 CTAACCC 991

RESULT 11
AUI17362
LOCUS AUI17362 HEMBA1 Homo sapiens CDNA clone HEMBA1001229 5', mRNA
DEFINITION sequence.
ACCESSION AUI17362
VERSION AUI17362.1 GI:10932324
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 889)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
HRI human cdna project

```

JOURNAL
COMMENT

Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp

HRI human CDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute

FEATURES
source

Location/Qualifiers
1..889
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEMBA1001229"
/clone_lib="HEMBA1"
/tissue_type="whole embryo, mainly head"
/dev_stage="embryo, 10 weeks"
/note="Vector: pME18SFL3"

BASE COUNT 167 a 301 c 249 g 166 t 6 others
ORIGIN

Alignment Scores:

Pred. No.: 1.98e-105 Length: 889
Score: 1206.00 Matches: 230
Percent Similarity: 98.71% Conservative: 0
Best Local Similarity: 98.71% Mismatches: 3
Query Match: 48.49% Indels: 1
DB: 9 Gaps: 0

US-09-899-422A-2 (1-455) x AUI17362 (1-889)

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QY 223 CysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLysSerLys 242
DB 3 TCCTTTTATCCCTCTCTCTCATTTGTTTAAATGATACGCTACCAAGTGGAGTCAAG 62
QY 243 LeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyLeuGluGlyThr 262
DB 63 CTCCTACTCCATTGTTTGTGGAAATCGACACCTGAAAGAGGGGAGCTTGAAGNACT 122
QY 263 ThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThrProThr 282
DB 123 ACTACTAAGCCCTGGCCCCNAACCAAGCTTCAGTCCACCTCCAGCTTACCCCAAC 182
QY 283 LeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThrProGly 302
DB 183 CTGGGCTTCAGTCCCGTGCAGTTCACCTTCACCTCCAGCTCCACCTATACCCCGGT 242
QY 303 AspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGlyAlaAsp 322
DB 243 GACTGTCCCACTTTTGGGCTCCCGCTCCCGACAGAGGTGGCACCACCTATCAGGGGTGAC 302
QY 323 ProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLysTrpGlu 342
DB 303 CCCATCTTGGACAGCCCTCCGCTCCGACCCCATCCCAACCCCTTCAGAGTGGAG 362
QY 343 AspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyrAlaVal 362
DB 363 GACAGGCCCAAGCAGCAGACCTAGACACTGATGACCCCGCAGCGCTGTACGCCGTG 422
QY 363 ValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeuSerAsp 382
DB 423 GTGGAGAACGTGCCCGCTTGGCTGGAGGAATTCGTGGCGCGCTAGGCGCTAGCGGAC 482
QY 383 HisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGlnTyrSer 402
DB 483 CACGAGATGATCGGTGGAGCTGCAGAACGGCGCTGCTGCGCGAGCGCAATACAGC 542
QY 403 MetLeuAlaThrTrpArgArgThrProArgArgGluAlaThrLeuGluLeuGly 422
DB 543 ATGCTGGCACCTGGAGGGCGGCCACCGCCGCGGAGGCCACCGCTGGAGCTGCTGGGA 602

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/db_xref="taxon:9606"
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/tissue_type="squamous cell carcinoma"
/lab_host="PH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 134 a 254 c 198 g 132 t
ORIGIN

Alignment Scores:
Pred. No.: 1,44e-104 Length: 718
Score: 1195.50 Matches: 227
Percent Similarity: 95.38% Conservative: 0
Best Local Similarity: 95.38% Mismatches: 10
Query Match: 48.07% Indels: 1
DB: 12 Gaps: 1

US-09-899-422a-2 (1-455) x BG680679 (1-718)
QY 219 PhePheGlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArg 238
DB 2 TTCTTGGTCTTGGCTTTATCCCTCTCTCATTTGGTTTATGTATCGCTACCAACGG 61
QY 239 TrpLysSerLysLeuTyrSerIleValCysGlyLysSerThrProGlyLysGluGlyGlu 258
DB 62 TGGNAGTCCCAAGCTCTACTCCATTGTTTGGGAATCGACACCTGAAAGAGGGGAG 121
QY 259 LeuGluGlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGly 278
DB 122 CTTGAGGAAGTACTACTAAGCCCTTGGCCCAACCAAGCTTCACTCCACCTCCAGCG 181
QY 279 PheThrProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerThr 298
DB 182 TTCACCCCAACCTGGGCTTACGTCGCGCCAGTTCACCTTCCAGCTCCACCC 241
QY 299 TyrThrProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyr 318
DB 242 TATACCCCGGTGACGTGCCAACTTTCGGGCTCCCGCAGAGAGTGCGCACCACTAT 301
QY 319 GlnGlyAlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeu 338
DB 302 CAGGGGGCTGACCCCATCTTGGCAGACCCCTGCGCTCCGACCCCAATCCCTT 361
QY 339 GlnLysTrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThr 358
DB 362 CAGAGTGGGAGGACAGCCGCCACACAGCCACAGAGCTAGACACTGATGACCCCGGAGC 421
QY 359 LeuTyrAlaValAlaGluAsnValProProLeuArgTyrTrpLysGluPheValArgArgLeu 378
DB 422 CTGTAGCGCTGTGTGAGAACGTGCCCGCTGCTGGAGGAATTCGTGGCGCCCTA 481
QY 379 GlyLeuSerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGlu 398
DB 482 GGCTGAGGAGACACAGATCGATCGCTGGAGCTGCAAGCGGCGCTGCTCGCGAG 541
QY 399 AlaGlnTyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeu 418
DB 542 GCGCATACAGCATGTGTGGACCTGGAGCGGCGCACCGCGCGGCGGAGCCAGCGCTG 601
QY 419 GluLeuLeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGlu 438
DB 602 GAGCTGCTGGAGCGCTGCTCGCGACATGGACCTGCTGGCTGCTGGAGGACATCGA 661
QY 439 GluAlaLeuCysGlyProAlaAlaLeuPro---ProAlaProSerLeuLeuArg 455
DB 662 GGAGCGCTTGGGGCCCCCGCCGACCTCCGACCGCCGCGCAGATCTTCTCAGA 715

RESULT 14
BM742388

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LOCUS BM742388 669 bp mRNA linear EST 01-MAR-2002
DEFINITION K-EST0015256 S6SNU620 Homo sapiens cDNA clone S6SNU620-5-C12 5', mRNA sequence.
ACCESSION BM742388
VERSION BM742388.1 GI:19063703
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 669)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 5 row: C column: 12
High quality sequence stop: 669.
Location/Qualifiers
1. 669
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-5-C12"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/lab_host="Top10P"
/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 128 a 239 c 193 g 109 t
ORIGIN

Alignment Scores:
Pred. No.: 1.79e-104 Length: 669
Score: 1194.00 Matches: 223
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.01% Indels: 0
DB: 14 Gaps: 0

US-09-899-422a-2 (1-455) x BM742388 (1-669)
QY 230 IleGlyLeuMetTyrArgTyrGlnArgTrpLysSerLysLeuTyrSerIleValCysGly 249
DB 1 ATTGGTTTATGTATCGTACCAACGGTGGAGTCCAAAGCTCTACTCCATTGTTGGG 60
QY 250 LysSerThrProGlyLysGluGlyGluLeuGluGlyThrThrThrLysProLeuAlaPro 269
DB 61 AATCGACACCTGAAAAGAGGGGGAGCTTGAGGAACTACTACTAAGCCCTTGGCCCCA 120

QY 270 AsnProSerPheSerProThrProGlyPheThrProThrLeuGlyPheSerProValPro 289
 Db 121 AACCAAGCTTCAGTCCACATCCAGGCTTACCCGCCACCTCGGCTTCAGTCCGCGCC 180
 QY 290 SerSerThrPheThrSerSerSerThrThrProGlyAspCysProAsnPheAlaA 309
 Db 181 AGTTCACCTTCACCTCAGCTCACCTATACCCCGGTGACTGTCCCACTTTGCGGCT 240
 QY 310 ProArgArgGluValAlaProProTyrglnGlyAlaAspProIleLeuAlaThrAlaLeu 329
 Db 241 CCCCGCAGAGAGTGGCACCACCTATACAGGGGCTGACCCCATCTTGGCAGACCCCTC 300
 QY 330 AlaSerAspProIleProAsnProLeuGlnLysTrpGluAspSerAlaHisLysProGln 349
 Db 301 GCCTCCGACCCCATCCCAACCCCTTCAGAAAGTGGGAGGACAGCGCCCAAGCCACAG 360
 QY 350 SerLeuAspThrAspAspProAlaThrLeuThrAlaValAlaValGluAsnValProLeu 369
 Db 361 AGCTAGACACTGATGACCCCGGACGCTGTACCGCGTGGTGGAGACGTGCCCGCTTG 420
 QY 370 ArgTrpLysGluPheValArgLeuGlyLeuSerAspHisGluIleAspArgLeuGlu 389
 Db 421 CGCTGGAAGGAATTCGTGGCGCGCTAGGGCTGAGCGCACGACGATCGCTGGCTGGAG 480
 QY 390 LeuGlnAsnGlyArgCysLeuArgGluAlaGlnTrpSerMetLeuAlaThrTrpArgArg 409
 Db 481 CTGCAGAACGGGCGCTGCTCGCGGAGCGCATACAGCATGCTGGCGACCTGGAGGCGG 540
 QY 410 ArgThrProArgArgGluAlaThrLeuGluLeuLeuGlyArgValLeuArgAspMetAsp 429
 Db 541 CGCAGCGCGCGCGGAGCGCCACCTGAGCTGTGGACGCGTGTCCCGGACATGGAC 600
 QY 430 LeuLeuGlyCysLeuGluAspIleGluAlaLeuCysGlyProAlaAlaLeuProPro 449
 Db 601 CTGCTGGGCTGCTGGAGGACATCGAGAGGCGCTTTGGGCGCGCGCGCTCCCGGCC 660
 QY 450 AlaProSer 452
 Db 661 GCGCCCACT 669

RESULT 15
 AL522989
 LOCUS AL522989 LTI_NFL004_NBC2 837 bp mRNA linear EST 13-FEB-2001
 DEFINITION prime, mRNA sequence.
 ACCESSION AL522989
 VERSION AL522989.1 GI:12786482
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 TITLE L1.W.B., Gruber, C., Jesses, J. and Polayes, D.
 FULL-LENGTH cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 CONTACT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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 /db_xref="taxon:9606"
 /clone="CS0DB009Yp14"
 /clone_lib="LTI_NFL004_NBC2"
 /sex="male"
 /tissue_type="neuroblastoma cells"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(GT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6"

vector. Library was normalized. Library was constructed by Life Technologies, Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com>*

BASE COUNT 199 a 231 c 229 g 177 t
 ORIGIN

Alignment Scores:
 Pred. No.: 4.97e-104 Length: 837
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 Percent Similarity: 99.53% Conservative: 0
 Best Local Similarity: 99.53% Mismatches: 1
 Query Match: 47.89% Indels: 0
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 Db 318 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAAAATAATTCGATTTGCTGTACC 377
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Job time : 1573 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 8, 2003, 22:41:48 ; Search time 92 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 28 | 424.4 | 31.0 | 1202 | 4 | US-08-804-166-3 | Sequence 3, Appli |
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ALIGNMENTS

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; Sequence 1, Application US/09106038A
; Patent No. 6007995
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker and Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Isis Pharmaceuticals, Inc.
; STREET: 2292 Faraday Avenue
; CITY: Carlsbad
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09106,038A
; FILING DATE: June 26, 1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Laurel Spear Bernstein
; REGISTRATION NUMBER: 37,280
; REFERENCE/DOCKET NUMBER: RTS-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (760) 931-9200
; TELEFAX: (760) 503-3820
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-106-038A-1

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Best Local Similarity 99.9%; Pred. No. 0;
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RESULT 2
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; Sequence 3, Application US/09505250A
; Patent No. 6329148
; GENERAL INFORMATION:
; APPLICANT: Rosen, Glenn
; APPLICANT: Kao, Peter
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
; TITLE OF INVENTION: Triptolides and Death Domain Ligands
; FILE REFERENCE: SUN-109PRV2
; CURRENT APPLICATION NUMBER: US/09/505,250A
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2161
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (256)...(1623)
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QY 601 AATGTTAAGGGCACTGAGGACTCAGGACACACAGTGTGCTGCTGCTGCTGCTGCTGCT 650
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QY 721 TCCAGCTCTACCTCCATGTTTCTGGGAATCAGACACTGAAAGAGGGAGCTTGA 780
Db 976 TCCAGCTCTACCTCCATGTTTCTGGGAATCAGACACTGAAAGAGGGAGCTTGA 1035
QY 781 GGAACCTACTACTAAGCCCTGCGCCCAACCCCAAGCTTCAGTCCCACTCCAGCTTCACC 840
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RESULT 3

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; Sequence 1, Application US/08321668
; Patent No. 5665859
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; APPLICANT: VAREFOLOVEEY, Eugene
; APPLICANT: BATKIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
; NUMBER OF SEQUENCES: 42
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/321,668
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107268
; FILING DATE: 12-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2175 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 121 GATAGTGTGTGCTCCCAAGGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 180
Db 376 GATAGTGTGTGCTCCCAAGGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 435
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QY 241 TGAGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAACACCTCAGACACTGCCTC 300
Db 496 TGAGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAACACCTCAGACACTGCCTC 555
QY 301 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGATCTCTTCTTCACAGTGGAC 360
Db 556 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGATCTCTTCTTCACAGTGGAC 615
QY 361 CGGACACCGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 616 CGGACACCGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 675
QY 421 TTCAGTGTCTAATTCAGCCCTCTGCTCAATGGGACCGTGCACCTCTCTCTCCAGGAG 480
Db 421 TTCAGTGTCTAATTCAGCCCTCTGCTCAATGGGACCGTGCACCTCTCTCTCCAGGAG 480
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| QY | 421 | TTCCAGTGCCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCTCTCTCTCCAGGAG | 480 |
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| QY | 481 | AAACAGAACACCGTGTGCACCTGCCATGCAGGTTCCTTCTAAGAGAAAACGAGTGTGTC | 540 |
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| DB | 755 | AATGTTAAGGGCACTCAGGACTCAGGACACACAGTGTGTGCGCTGGTCATTTCCTTT | 814 |
| QY | 661 | GGTCTTTGGCTTTTATCCCTCCTCTTCATTGGTTTAAATGATCGCTACCAACGGTGGAA | 720 |
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| DB | 875 | TCCAAGCTCTACTCCATTGTTGTGGGAATCACAACCTGAAAAGAGGGGAGCTTGAA | 934 |
| QY | 781 | GGAACTACTACTAAGGCCCTTGGCCCCAAACCCCAAGCTTCAGTCCCACTCCAGGCTTCACC | 840 |
| DB | 935 | GGAACTACTACTAAGGCCCTTGGCCCCAAACCCCAAGCTTCAGTCCCACTCCAGGCTTCACC | 994 |
| QY | 841 | CGACCCCTGGGTTCAGTCCCGTGGCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC | 900 |
| DB | 995 | CGACCCCTGGGTTCAGTCCCGTGGCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC | 1054 |
| QY | 901 | CCGGTGACTGTCCCAACTTTGGGGTCCCGCCAGAGAGGTGSCACCACTATCAGGG | 960 |
| DB | 1055 | CCGGTGACTGTCCCAACTTTGGGGTCCCGCCAGAGAGGTGSCACCACTATCAGGG | 1114 |
| QY | 961 | GCTGACCCCATCCTTCGACAGCCCTCGCCTCCGACCCCATCCCAACCCCTTCAGAAG | 1020 |
| DB | 1115 | GCTGACCCCATCCTTCGACAGCCCTCGCCTCCGACCCCATCCCAACCCCTTCAGAAG | 1174 |
| QY | 1021 | TGGGAGGACAGCCCAAGCCACAGACGCTTAGACTGATGACCCCGGAGCGCTGTAC | 1080 |
| DB | 1175 | TGGGAGGACAGCTGCCACAAAGCCACAGACGCTTAGACTGATGACCCCGGAGCGCTGTAC | 1234 |
| QY | 1081 | GCCGTGTTGGAGAACGTGCCCGCTTGGCTTGAAGGAATTCGTGGGGCCCTAGGGCTG | 1140 |
| DB | 1235 | GCCGTGTTGGAGAACGTGCCCGCTTGGCTTGAAGGAATTCGTGGGGCCCTAGGGCTG | 1294 |
| QY | 1141 | AGGACCAAGATCATCGGTGGAGCTGTGAGAACGGGGGCTGTCTGTGCGGAGGCGCA | 1200 |
| DB | 1295 | AGGACCAAGATCATCGGTGGAGCTGTGAGAACGGGGGCTGTCTGTGCGGAGGCGCA | 1354 |
| QY | 1201 | TACAGCATCTCGGACCTTGGAGGCGGCGACGCCCGCGGAGGCCACGCTGGAGCTG | 1260 |
| DB | 1355 | TACAGCATCTCGGACCTTGGAGGCGGCGACGCCCGCGGAGGCCACGCTGGAGCTG | 1414 |
| QY | 1261 | CTGGGACCGCTCTCCGCGACATGGACCTGTCTGGGCTGCCTGGAGGACATCGAGGAGCG | 1320 |
| DB | 1415 | CTGGGACCGCTCTCCGCGACATGGACCTGTCTGGGCTGCCTGGAGGACATCGAGGAGCG | 1474 |
| QY | 1321 | CTTTGGGGCCCGCGGCCCTCCGCGCCGCGCCAGTCTTCTCAGATGA | 1368 |
| DB | 1475 | CTTTGGGGCCCGCGGCCCTCCGCGCCGCGCCAGTCTTCTCAGATGA | 1522 |

RESULT &

RESULT 8
DS-08-465-982-24

US-08-465-982-24
: Sequence 24, Application US/08465982

; Sequence Z4, Appl. No. 5863786
; Patent No. 5863786; PATENT NO. 3683786
; GENERAL INFORMATION:

APPLICANT: M. Feldmann, P.W. Gray,

APPLICANT: M.J.C. Turner, F.M. Brennan

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1  TITLE OF INVENTION:  Modified human TNFalpha (Tumor
2  TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
3  NUMBER OF SEQUENCES:  57
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE:  Reed & Robbins
6  STREET:  635 Bryant Street
7  CITY:  Palo Alto
8  STATE:  California
9  COUNTRY:  USA
10 ZIP:  94301
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE:  Floppy disk
14 COMPUTER:  IBM PC compatible
15 OPERATING SYSTEM:  PC-DOS/MS-DOS
16 SOFTWARE:  PatentIn Release #1.0, version #1.25
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER:  US/08/465,982
19 FILING DATE:
20 CLASSIFICATION:
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER:  US/08/050,319
23 FILING DATE:  10-May-1993
24 ATTORNEY/AGENT INFORMATION:
25 NAME:  Robbins, Roberta L.
26 REGISTRATION NUMBER:  33,208
27 REFERENCE/DOCKET NUMBER:  5150-0030
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE:  (415) 617-8999
30 TELEFAX:  (415) 327-3231
31 INFORMATION FOR SEQ ID NO:  24:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH:  2062 base pairs
34 TYPE:  nucleic acid
35 STRANDEDNESS:  double
36 TOPOLOGY:  linear
37 MOLECULE TYPE:  cDNA to mRNA
38 FEATURE:
39 NAME/KEY:  CDS
40 LOCATION:  155..1519
41
42 US-08-465-982-24

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| Best Local Similarity | 99.6%; | Pred. No. 0; | | |
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| OY | 1 | ATGGGGCTCTCCACCGTGCCTGACCTGTCTGCCACTGGTGCTCCTGTGGAGCTGTGGTG | 60 | |
| Db | 155 | ATGGGGCTCTCACCGTGCCTGNCTGTCTGCCCTGGTGCTCCTGTGGAGCTGTGGTG | 214 | |
| OY | 61 | GGAATATACCCCTCAGGGGGTTATTGGACCTGGTCCCCTCACTAGGGGACAGGGAGAAGAGA | 120 | |
| Db | 215 | GGAATATACCCCTCAGGGGGTTATTGGACCTGGTCCCCTCACTAGGGGACAGGGAGAAGAGA | 274 | |
| OY | 121 | GATAGTGTGTGTCCTCCAAAGAAAATAATATCCACCCTCAAATAAATTCGATTTCCTGTACC | 180 | |
| Db | 275 | GATAGTGTGTGTCCTCCNAGAAATAATATCCACCCTCAAATAAATTCGATTTCCTGTACC | 334 | |
| OY | 181 | AAGTGCACAAAAGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGAC | 240 | |
| Db | 335 | AAGTGCACAAAAGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGAC | 394 | |
| OY | 241 | TGCAGGGAGTGTGAGAGCGGCTCTTCACGGCTTCAGAAAACCACTCGACACTGCCTC | 300 | |
| Db | 395 | TGCAGGGAGTGTGAGAGCGGCTCTTCACGGCTTCAGAAAACCACTCGACACTGCCTC | 454 | |
| OY | 301 | AGCTGCTCCAATGCCGAANGAAATGGGTCAAGTGGAGATCTCTTCTTCACAGTGGAC | 360 | |
| Db | 455 | AGCTGCTCCAATGCCGAANGAAATGGGTCAAGTGGAGATCTCTTCTTCACAGTGGAC | 514 | |
| OY | 361 | CGGGACACCGTGTGTGGCTGCAGGAAGAACCACTACCGCATTTATGGAGTGAACACCTT | 420 | |
| Db | 515 | CGGGACACCGTGTGTGGCTGCAGGAAGAACCACTACCGCATTTATGGAGTGAACACCTT | 574 | |


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Db 576 ACTCAGAACCGGTGTAACTGCGCATCGAGGGTCTTTCTGAGAGAAAGTGAAGTGCCTC 635
Qy 541 TCCTGTAGTAACTGAAGAAAGCCGTGAGTGCAGAAAGTGTGCTA---CCCGAGATT 597
Db 636 CTTGACACCACTGCAAGAAAGAGAGAGTGTATGAAGTGTGCTACCTCCTCCGCTT 595
Qy 598 GAGAAATGAAGGCACTGAGGACTCAGGACCAAGCTGCTGTGCTGCTGCTGCTGCTGCT 657
Db 696 GCAATGTACAAACCCCGAGGACTCAGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 755
Qy 658 TTTGGCTTTCCTGCTTATCCCTCCTCTCTCATTTGTTTAAATGATATGCTACCAAGGCTG 717
Db 756 CTAGTCTTTCCTTCTATCTTCTTCTTCTATCTATCTATCTATCTATCTATCTATCTAT 815
Qy 718 AAGTCCAAAGCTCTACTCCATCTGTTGTTGGGAAATGACACCTGAAAGAGAGGGAGCTT 777
Db 816 AGGCCGGAAGTCTACTCCATCATTTGTAGGATCCCGTCCCTGCTGCTGCTGCTGCTGCT 875
Qy 778 GAAGAACTACTACTAAGCCCTCGGCCCAAGCCCAAGCTTCACTGCTGCTGCTGCTGCTGCT 837
Db 876 GGAAGGCCCTTAAGT-----CCAGCCCTCCCGAGCTTCCAGCCCTCCAGCCCTCCGCTT 929
Qy 838 ACCCCACCTGCGGCTCAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
Db 930 ACCCCACCTGCGGCTTCCAGCCCTCCAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 989
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Db 990 AGCCCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1049
Qy 949 CCCTATCAGGGGCTGAGCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1008
Db 1050 ACC---CAGGGAGCTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1106
Qy 1009 CCCCTTCAAGAGTGGGAGCAGCGCCACACAGCCACAGAGCCCTAGACACTGATGACCC 1068
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Qy 1129 CGCTAGGCTGAGGACCAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1188
Db 1224 TTCATGGGCTGAGCGACAGAGATGAGAGGCTGAGAGTGCAGAACGGGCTGCTGCTGCT 1283
Qy 1189 CGCAGGCGCAATACAGATGCTGCGACCTGAGGCGGCGCGCGCGCGCGCGCGCGCGCG 1248
Db 1284 CGCAGGCTCAGTACAGCTGCTGAGAGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCG 1343
Qy 1249 ACCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1308
Db 1344 ACCTGGAAGTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1403
Qy 1309 ATCAGGAGGCGCTTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1338
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RESULT 10

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US-09-513-007-1
; Sequence 1, Application US/09513007
; Patent No. 6406907
; GENERAL INFORMATION:
; APPLICANT: Taylor, J. Michael
; APPLICANT: Kehrl, Jr., Marcus
; APPLICANT: Lee, Eun-Kyung
; APPLICANT: Kwang, Simon
; TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
; FILE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 08411-018001
; CURRENT APPLICATION NUMBER: US/09/513.007
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; CURRENT FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/122,156
; FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2440
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (294)...(1706)
US-09-513-007-1
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Query Match

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Best Local Similarity 50.1%; Score 685.4; DB 4; Length 2440;
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Db 294 ATGGGCTCTCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 353
Qy 61 GGAATATACCCCTCAGGGGTTATGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 354 GATGTGTACCCCGCAGGGGTTTCAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 413
Qy 121 GATAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 414 GAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
Qy 181 AAGTGCACAAAGGAACACTTGTACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 474 AAGTGCACAAAGGATACCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533
Qy 241 TGCAGGAGTGTGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 534 TGCAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593
Qy 301 AGCTGCTCAAAATCCGAAAGAAATGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 594 AGCTGCTCAAGTCCGCGGAGAAATGTTCCAGGTGAGATTTCCGCTTGTGTAGTGGAC 653
Qy 361 CGGACACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 654 CGGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 713
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Qy 481 AAACAGAACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
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Db 834 TCCGTGTAGTAACTGTAAGAAAGCTGAGTGCAGAAAGTGTGCTGCTGCTGCTGCTGCTGCT 890
Qy 601 AATGTTAAGGCACTGAGGACTCAGGACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 891 ACTGGTAAAGACTCTCAGGACCCAGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 950
Qy 661 GGTCTTTGCTTTTATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319
FILING DATE: 10-May-1993
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..597
US-08-465-982-47

Query Match 43.4%; Score 593.6; DB 2; Length 600;
Best Local Similarity 99.3%; Pred. No. 3.4e-133;
Matches 596; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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| QY | 1 | ATGGCCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCTCCTCGAGCTGTGGTG | 60 |
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| QY | 61 | GGATATATACCCCTCAGGGGTTATTCGACTGGTCCCTACCTAGGGGACAGGAGAGAGA | 120 |
| Db | 61 | GGATATATACCCCTCAGGGGTTATTCGACTGGTCCCTACCTAGGGGACAGGAGAGAGA | 120 |
| QY | 121 | GATAGTGTGTGCCCAAGGAAATATATCCACCTCAAAATATTCGATTGCTGTACC | 180 |
| Db | 121 | GATAGTGTGTGCCCAAGGAAATATATCCACCTCAAAATATTCGATTGCTGTACC | 180 |
| QY | 181 | AAGTCCCAAGAGAACCTACTGTGTACATGACTGTCCAGGCCCGGGGAGGATACGGAC | 240 |
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| QY | 241 | TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAACCACCTCAGACACTGCCTC | 300 |
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| Db | 301 | AGCTGCTCCAAATGCCGAAGGAATGGGTGAGTGGAGATCTCTTCTTGCACAGTGGAC | 360 |
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Job time : 97 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2003, 01:17:59 ; Search time 185 Seconds
(without alignments)
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Title: US-09-899-422a-2

Perfect score: 2487

Sequence: 1 MGLSTVPDLLLVLELLV.....DIEEALCGPALPPAPSLLR 455

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Delop 6.0 , Delext 7.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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6: /cgn2_6/ptodata/2/pubpna/PCT07_PUBCOMB.seq.*
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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 2 | 2487 | 100.0 | 1368 | 9 US-09-899-429A-1 | Sequence 1, Appl1 |
| 3 | 2487 | 100.0 | 1368 | 9 US-09-792-356-1 | Sequence 1, Appl1 |
| 4 | 2487 | 100.0 | 1368 | 10 US-09-899-422-1 | Sequence 1, Appl1 |

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| 5 | 2487 | 100.0 | 2111 | 10 US-09-880-107-2360 | Sequence 2360, Ap |
| 6 | 2487 | 100.0 | 2141 | 9 US-09-898-234-16 | Sequence 16, Appl |
| 7 | 2487 | 100.0 | 2141 | 9 US-09-899-429A-26 | Sequence 26, Appl |
| 8 | 2487 | 100.0 | 2141 | 9 US-09-792-356-16 | Sequence 16, Appl |
| 9 | 2487 | 100.0 | 2141 | 10 US-09-899-422-16 | Sequence 16, Appl |
| 10 | 2487 | 100.0 | 2175 | 12 US-10-120-397-1 | Sequence 1, Appl1 |
| 11 | 2481 | 99.8 | 1368 | 9 US-10-352-408-3 | Sequence 3, Appl1 |
| 12 | 2069 | 83.2 | 1334 | 9 US-09-898-234-11 | Sequence 11, Appl |
| 13 | 2069 | 83.2 | 1334 | 9 US-09-792-356-11 | Sequence 11, Appl |
| 14 | 2069 | 83.2 | 1334 | 10 US-09-899-422-11 | Sequence 11, Appl |
| 15 | 2055 | 82.6 | 1334 | 9 US-09-899-429A-21 | Sequence 21, Appl |
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| 17 | 1550.5 | 62.3 | 2173 | 9 US-09-898-234-14 | Sequence 14, Appl |
| 18 | 1550.5 | 62.3 | 2173 | 9 US-09-899-429A-24 | Sequence 24, Appl |
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| 20 | 1550.5 | 62.3 | 2173 | 10 US-09-899-422-14 | Sequence 14, Appl |
| 21 | 1517 | 61.0 | 2440 | 10 US-09-970-532-1 | Sequence 1, Appl1 |
| 22 | 1192 | 47.9 | 633 | 9 US-09-899-429A-7 | Sequence 7, Appl1 |
| 23 | 1141 | 45.9 | 603 | 9 US-09-899-429A-13 | Sequence 13, Appl |
| 24 | 1117.5 | 44.9 | 600 | 9 US-09-899-429A-11 | Sequence 11, Appl |
| 25 | 1066.5 | 42.9 | 570 | 9 US-09-899-429A-17 | Sequence 17, Appl |
| 26 | 1051 | 42.3 | 549 | 9 US-09-899-429A-9 | Sequence 9, Appl1 |
| 27 | 1016 | 40.9 | 1301 | 10 US-09-756-186-7 | Sequence 7, Appl1 |
| 28 | 1000 | 40.2 | 519 | 9 US-09-899-429A-15 | Sequence 15, Appl |
| 29 | 995.5 | 40.0 | 1147 | 10 US-09-756-186-5 | Sequence 5, Appl1 |
| 30 | 992 | 39.9 | 516 | 9 US-09-899-429A-19 | Sequence 19, Appl |
| 31 | 941 | 37.8 | 483 | 9 US-09-898-234-3 | Sequence 3, Appl1 |
| 32 | 941 | 37.8 | 483 | 9 US-09-899-429A-3 | Sequence 3, Appl1 |
| 33 | 941 | 37.8 | 483 | 9 US-09-792-356-3 | Sequence 3, Appl1 |
| 34 | 941 | 37.8 | 483 | 9 US-09-882-735-1 | Sequence 1, Appl1 |
| 35 | 941 | 37.8 | 483 | 10 US-09-899-422-3 | Sequence 3, Appl1 |
| 36 | 941 | 37.8 | 483 | 10 US-09-907-263-1 | Sequence 1, Appl1 |
| 37 | 941 | 37.8 | 486 | 9 US-09-899-429A-5 | Sequence 5, Appl1 |
| 38 | 909.5 | 36.6 | 1674 | 9 US-09-359-595-12 | Sequence 12, Appl |
| 39 | 870.5 | 35.0 | 1202 | 10 US-09-756-186-3 | Sequence 3, Appl1 |
| 40 | 852 | 34.3 | 1049 | 10 US-09-756-186-1 | Sequence 1, Appl |
| 41 | 843 | 33.9 | 479 | 9 US-10-043-487-100 | Sequence 100, App |
| 42 | 790 | 31.8 | 507 | 9 US-09-911-904-129 | Sequence 129, App |
| 43 | 766.5 | 30.8 | 5870 | 10 US-09-838-718A-8 | Sequence 8, Appl1 |
| 44 | 738.5 | 29.7 | 543 | 10 US-09-970-532-3 | Sequence 3, Appl1 |
| 45 | 638 | 25.7 | 339 | 9 US-09-882-735-5 | Sequence 5, Appl1 |

ALIGNMENTS

RESULT 1
US-09-898-234-1
; Sequence 1, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98,385-1
; CURRENT APPLICATION NUMBER: US/09/898,234
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1368

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1
 LENGTH: 1368
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1365)
 NAME/KEY: sig_peptide
 LOCATION: (1)..(87)
 NAME/KEY: misc_feature
 LOCATION: (88)..(120)
 OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
 OTHER INFORMATION: extracellular proteases following secretion
 NAME/KEY: misc_feature
 LOCATION: (606)..(633)
 OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
 OTHER INFORMATION: extracellular proteases following secretion
 US-09-899-429A-1

Alignment Scores:
 Pred. No.: 5,82e-251 Length: 1368
 Score: 2487.00 Matches: 455
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-899-422A-2 (1-455) x US-09-899-429A-1 (1-1368)

QY 1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuLeuVal 20
 DB 1 ATGGGCTCTCCACCGTGGCTGCTGCTGCCACTGCTGCTGGAGCTGTGGTG 60
 QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGluAspArgGluLysArg 40
 DB 61 GGAAATATACCCCTCAGGGGTATTGACATGGTCCCTTACCTAGGGACAGGGAAGAAGA 120
 QY 41 AspSerValCysProGlnGlyTyrIleHisProGlnAsnSerIleCysCysThr 60
 DB 121 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAAAATAATTCGATTTCGTACC 180
 QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
 DB 181 AAGTGGCACAAGAGAACCTTACTTGTACAAATGACTGTCCAGGGCCCGGGCAGGATACGGAC 240
 QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
 DB 241 TGCAGGGAGTGTGAGAGGGCTCTTCACCGCTTCAGAAACACCTCAGACACTGCCCTC 300
 QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
 DB 301 AGCTGCTCCAAATGCCGAAGGAAATGGGTGAGTGGAGATCTCTTCTTGCACAGTGGAC 360
 QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
 DB 361 CGGGACACCGTGTGGTGCAGGAAGAACACCTACCGGCATATTGGAGTGAACACCTT 420
 QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
 DB 421 TTCCAGTGTCTCAATTTGCACCTCTGCCCTCAATGGGACCGTGCACCTCTCCTCCAGGAG 480
 QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
 DB 481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTAAGAGAAACAGAGTGTGTC 540
 QY 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
 DB 541 TCCTGTAGTAACCTGTAAAGAAACCTTGGAGTGCACGAAGTGTGCTACCCCAATGAG 600
 QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
 DB 601 AATGTTAAGGGCACTGAGGACTCAGGCACACAGTGTGTGGCCCTGGTCACTTTCTTT 660

QY 221 GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTyrLys 240
 DB 661 GGTCCTTGGCTTTTATCCCTCTCTTCATTGGTTTAAATGATCGCTACCAACGGTGAAG 720
 QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGluLeuGlu 260
 DB 721 TCCAGCTCTACTCCATTGTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGAA 780
 QY 261 GlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
 DB 781 GGAACTACTACTAAGCCCTTGGCCCAACCCCAAGCTTCAGTCCCTACTCCAGCTTCACC 840
 QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr 300
 DB 841 CCCACCTTGGCTTTCAGTCCGCTGCGCCAGTTCACCTTCCCTCCAGCTCCACCTATACC 900
 QY 301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly 320
 DB 901 CCGGTGACTGTCCCAACTTTGCGGCTCCCGCAGAGAGTGGCACCACCTATCAGGGG 960
 QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
 DB 961 GCTGACCCCTATCTTGGACAGCCCTCGCTCCGACCCCTCCCAACCCCTTCAGAAG 1020
 QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
 DB 1021 TGGGAGGACAGCCGCCCAAGCCACAGAGCCCTAGACACTGATGACCCCGGAGCGCTGTAC 1080
 QY 361 AlaValValGluAsnValProProLeuArgTyrTrpLysGluPheValArgArgLeuGlyLeu 380
 DB 1081 GCGTGTGGAGAACCTGCCCCGTTCCGCTGGAAGAAATTCGTGGGGCCCTTAGGGCTG 1140
 QY 381 SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
 DB 1141 AGCAGCACAGATCGATCGCTGGAGCTGCAGACGGGCGCTGCTCGCGAGGCGCAA 1200
 QY 401 TyrSerMetLeuAlaThrTrpArgArgTyrProArgArgGluAlaThrLeuGluLeu 420
 DB 1201 TACAGCATGCTGGCGACCTGGAGGGCGCAGCCGCGCGGCGGAGCCAGCTGGAGCTG 1260
 QY 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
 DB 1261 CTGGGACGGTGTCTCCGACATGGACCTGCTGGGCTGCTGGAGACATCGAGGAGCG 1320
 QY 441 LeuCysGlyProAlaAlaLeuProAlaProSerLeuLeuArg 455
 DB 1321 CTTTGGGGCCCGCCCTCCCGCGCGCGCGCGCTCTCTCAGA 1365

RESULT 3

US-09-792-356-1

; Sequence 1, Application US/09792356

; Publication No. US20020183485A1

; GENERAL INFORMATION:

; APPLICANT: Hauptmann, Rudolph

; APPLICANT: Himmler, Adolph

; APPLICANT: Maurer-Fogy, Ingrid

; APPLICANT: Stratowa, Christian

; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for

; TITLE OF INVENTION: them

; FILE REFERENCE: 98,385-G

; CURRENT APPLICATION NUMBER: US/09/792,356

; CURRENT FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: 08/477,639

; PRIOR FILING DATE: 1995-06-07

; PRIOR APPLICATION NUMBER: 08/383,676

; PRIOR FILING DATE: 1995-02-01

; PRIOR APPLICATION NUMBER: 08/153,287

; PRIOR FILING DATE: 1993-11-17

; PRIOR APPLICATION NUMBER: 07/821,750

; PRIOR FILING DATE: 1992-01-02

; PRIOR APPLICATION NUMBER: 07/511,430

; PRIOR FILING DATE: 1990-04-20

QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
 DB 273 GGAATATACCCCTCAGGGGTATTTGAGCTGGTCCCTCACCCTAGGCGACAGGGAGAAGA 332
 QY 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
 DB 333 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCCTCAAAATAATTCGATTGCTGTACC 392
 QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
 DB 393 AAGTGCACAAAGAAACCTTACTTGTACAATGACTGCCAGGCGCGGCGAGGATACGGAC 452
 QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
 DB 453 TGCAGGAGGTGTGAGAGCGGCTCTTCACCGCTTCAGAAACACACCTCAGACACTGCCCTC 512
 QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValIleLysSerSerCysThrValAsp 120
 DB 513 AGCTGCTCCAAATGCCAAAGAAATGGGTGAGTGGAGATCTCTTCTTGCACAGTGGAC 572
 QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
 DB 573 CGGACACACCGTGTGTGGCTGCAGGAAGAACACAGTACCGCATTTATTGGAGTGAACCTT 632
 QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
 DB 633 TTCAGTGTCTCAATTTGACGCTCTGCCCTCAATGGGACCGTGCACCTCTCTGCCAGGAG 692
 QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPheLeuArgGluAsnGluCysVal 180
 DB 693 AAACAGACACCGTGTGCACCTGCCATGCAGGTTCTTCTTAAGAGAAACAGAGTGTGTC 752
 QY 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
 DB 753 TCCTGTAGTAACCTGTAAAGAAACCTGGAGTGCACGAAGTGTGCTACCCAGATTTAG 812
 QY 201 AsnValIleGlyThrGluAspSerGlyThrValLeuLeuProLeuValIlePhePhe 220
 DB 813 AATGTTAAGGCACTGAGGACTCAGGACACACAGTGTGTGCCCTGGTCAATTTCTTT 872
 QY 221 GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
 DB 873 GGTCCTTTCCTTTATCCCTCTCTTCATTGTTTAAATGATGCTACCAACCGGTGAAG 932
 QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyLeuLeuGlu 260
 DB 933 TCCAAGCTCTACTCCATTGTTGTGGGAATTCGACACCTGAAAGAGGGGAGCTTGAA 992
 QY 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
 DB 993 GGAACCTACTACTAAGCCCTTGGCCCAACCCCAAGCTTCAGTCCCACTCCAGGCTTCACC 1052
 QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr 300
 DB 1053 CCCACCTGGGCTTACGTCCGTCGCGCCAGTTCACCTTCACCTCCAGCTCCACCTATACC 1112
 QY 301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly 320
 DB 1113 CCGGGTGACTGTCCCAACTTGGGGCTCCCGCAGAGAGGTGGCACCACTATCAGGGG 1172
 QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
 DB 1173 GCTGACCCCACTTCGGACAGCCCTCGCCCTCCGACCCCACTCCCAACCCCTTCAGAAG 1232
 QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
 DB 1233 TGGAGAGACAGCCGCCACAGCCACAGAGCCTAGACACTGATGACCCCGGAGCGTGTAC 1292
 QY 361 AlaValValGluAsnValProProLeuArgTyrTrpLysGluPheValArgArgLeuGlyLeu 380
 DB 1293 GCGGTGTGGAGAACGTGCCCGCTTGCCTGGAAGGAATTCGTGGCGGCCCTAGGCGCTG 1352
 QY 381 SerAspHisGlnIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400

DB 1353 AGCGACACAGATCCATCGCTGGAGCTGCAGAACGGGCGCTGCCTGCCGAGGCGCAA 1412
 QY 401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420
 DB 1413 TACAGCATGCTGGCGACCTGGAGGCGCGCACCGCGGCGGAGCCACGCTGGAGCTG 1472
 QY 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
 DB 1473 CTGGGAGCGGTGCTCCGCGACATGGACCTGCTGGCTGCTGGAGGACATCGAGGAGCG 1532
 QY 441 LeuCysGlyProAlaAlaLeuProAlaProSerLeuLeuArg 455
 DB 1533 CTTTGGGCGCCCGCGCCCTCCCGCGCGCGCGCGCTTCTCTCAGA 1577
 RESULT 9
 US-09-899-422-16
 ; Sequence 16, Application US/09899422
 ; Patent No. US20020090676A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hauptmann, Rudolph
 ; APPLICANT: Himmler, Adolph
 ; APPLICANT: Maurer-Fogy, Ingrid
 ; APPLICANT: Stratowa, Christian
 ; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
 ; TITLE OF INVENTION: Them
 ; FILE REFERENCE: 98,385-H
 ; CURRENT APPLICATION NUMBER: US/09/899,422
 ; CURRENT FILING DATE: 2001-08-21
 ; PRIOR APPLICATION NUMBER: 09/525,998
 ; PRIOR FILING DATE: 2000-03-15
 ; PRIOR APPLICATION NUMBER: 08/383,676
 ; PRIOR FILING DATE: 1995-02-01
 ; PRIOR APPLICATION NUMBER: 08/153,287
 ; PRIOR FILING DATE: 1993-11-17
 ; PRIOR APPLICATION NUMBER: 07/821,750
 ; PRIOR FILING DATE: 1992-01-02
 ; PRIOR APPLICATION NUMBER: 07/511,430
 ; PRIOR FILING DATE: 1990-04-20
 ; NUMBER OF SEQ ID NOS: 87
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 16
 ; LENGTH: 2141
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (213)..(1580)
 ; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
 ; OTHER INFORMATION: ITNF-R2
 US-09-899-422-16
 Alignment Scores:
 Pred. No.: 1,14e-250 Length: 2141
 Score: 2487.00 Matches: 455
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
 US-09-899-422A-2 (1-455) x US-09-899-422-16 (1-2141)
 QY 1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuLeuVal 20
 DB 213 ATGGGCTCTCCACCGTCCCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 272
 QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
 DB 273 GGAATATACCCCTCAGGGGTATTTGAGCTGGTCCCTCACCCTAGGCGACAGGGAGAAGA 332
 QY 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
 DB 333 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCCTCAAAATAATTCGATTGCTGTACC 392

| | | | |
|------|----|---|------|
| 316 | Db | GGAAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAAGACA | 375 |
| 41 | QY | ASerValCysProGlnGlyLysTryIleHisProGlnAsnAsnSerIleCysCysThr | 60 |
| 376 | Db | GATAGTGTGTGCCCAAGGAAATATATCCACCCTCAAAATAATTTCGATTTCTGTACC | 435 |
| 61 | QY | LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp | 80 |
| 436 | Db | ARGTGGCCAAAGAACCTACTTTGTACAATGACTGCCAGGCCCGGGGAGGAGTAGCGGAC | 495 |
| 81 | QY | CysArgGluCysGlnSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu | 100 |
| 496 | Db | TGCAGGAGGTGAGACGGCTCTCTCCACCGCTTCAGAAAACCACTTCAGACACTGCCTC | 555 |
| 101 | QY | SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp | 120 |
| 556 | Db | AGTGTCTCCAAATGCCGAAGGAAATGGGTCAAGTGGAGATCTCTTTGCACAGTGGAC | 615 |
| 121 | QY | ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu | 140 |
| 616 | Db | CGGGACACCGTGTGTGCTCGAGGAAGAACCACTACCGGCATTATTGGAGTGAACACCTT | 675 |
| 141 | QY | PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu | 160 |
| 676 | Db | TTCCAGTGTCTCAATTGCACCGCTGCGCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG | 735 |
| 161 | QY | LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal | 180 |
| 736 | Db | AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTAGAGANAAACGAGTGTGC | 795 |
| 181 | QY | SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu | 200 |
| 796 | Db | TCCTGTAGTAACTGTAAGAAAGCCTGGAGTCGACGAAGTGTGTGCTACCCAGATTGAG | 855 |
| 201 | QY | AsnValLysGlyThrGluAspSerSerGlyThrThrValLeuLeuProLeuValIlePhePhe | 220 |
| 856 | Db | AAITGTTAAGGGGACTGAGGACTCAGGACCACACAGTGTGTGCCCCGGTCATTTCTTT | 915 |
| 221 | QY | GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys | 240 |
| 916 | Db | GGCTTTGGCCTTTATCCCTCCCTTCATTGGTTTAATGTATCGCTACCAACCGTGGAG | 975 |
| 241 | QY | SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGlnLeuGlu | 260 |
| 976 | Db | TCCAAGCTCTACTCCATTGTTTGTGGAAATCGACACCTGAAAGAGGGGGAGCTTGA | 1035 |
| 261 | QY | GlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr | 280 |
| 1036 | Db | GGAACTACTACTAAGCCCCCTGGCCCCAAACCCAAAGCTTCAGTCCCACTCCAGGCTTCAC | 1095 |
| 281 | QY | ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr | 300 |
| 1096 | Db | CCCACCTGGGCTTCAGTCCCGTGCCAGTTCACCTTCACCTCCAGCTCCACCTATACC | 1155 |
| 301 | QY | ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly | 320 |
| 1156 | Db | CCCGGTGACTGTCCCAACTTTGGCGCTCCCGCAGAGAGGTGGCACCCACTATCAGGGG | 1215 |
| 321 | QY | AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys | 340 |
| 1216 | Db | GCTGAACCCCATCCTTGGCGACAGCCCTCGCTCGACCCCACTCCCAACCCCTTCAGAAG | 1275 |
| 341 | QY | TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr | 360 |
| 1276 | Db | TGGGAGACAGGCCCAACAGCCACAGAGCTTAGACACTGATGACCCCGGACGCTGTAC | 1335 |
| 361 | QY | AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgLeuGlyLeu | 380 |
| 1336 | Db | GCCGTGTGGAGAACGTGCCCGCTTCGGCTGGAGGAATTCGTGGCGCGCTAGGCGCTG | 1395 |
| 381 | QY | SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln | 400 |
| 1396 | Db | AGCCACCAACAGATTCGATCGCTGGAGCTGCAGAACGGCGCTGCTGCGCAGGCGCAA | 1455 |

Db 61 GGAATATACCCCTCAGGCGGTATTTGGACTGGTCCCTCACCTAGGGGACAGGAGAGAGA 120
Qy 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
Db 121 GATAGTGTGTGCCCAAGGAATAATATCCACCTCAATAATTCGATTGCTGTACC 180
Qy 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
Db 181 AAGTGCCCAAGGAAGCACTACTGTACAAATGACTGTCCAGGCGCGGGGAGGATACGGAC 240
Qy 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
Db 241 TCCAGGGAGTGTGAGCGGGCTCTTCCACCGCTTCAGAAACACCTCAGACATGCGCTC 300
Qy 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
Db 301 AGCTGCTCCAAATGCCGAAGGAATAGTGTGAGTGGAGATCTCTTCTTGACAGTGGAC 360
Qy 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
Db 361 CGGGACACCGTGTGTGGTGTGAGGAAGAACAGTACCGGCATATTATGGAGTGAACACCT 420
Qy 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
Db 421 TTCAGTGTCTCAATGTGAGCTCTGCTCAATGGGACCGTGCACCTCTCTCGCCAGGAG 480
Qy 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
Db 481 AAACAGAACACCGTGTGACCTGCCATGCGATGCTTCTTCTTAAGAGAAACAGTGTGTC 540
Qy 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
Db 541 TCCTGTACTACTGTAAAGAAAGCGTGGAGTGCAGAGTGTGCTTACCCACAGATTGAG 600
Qy 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
Db 601 AATGTTAAGGACATGAGGACTCAGGCACACAGTGTGTGCCCCCTGGTCAATTTCTTT 660
Qy 221 GlyLeuCysLeuLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
Db 661 GGTCTTTGCCTTTATCCCTCTCTCTCATTTGTTTAAAGTTATCGTACCAACGGTGGAG 720
Qy 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyClnLeuGlu 260
Db 721 TCCAAGCTCTACTCCATGTTGTGGAAATCGACACCTGAAAGAGGGGAGCGTTGAA 780
Qy 261 GlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
Db 781 GGACTACTACTAAGCCCTCGGCCCAACCAAGCTTCAGTCCACCTCCAGGCTTACC 840
Qy 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerThrTyrThr 300
Db 841 CCCACCTGGGCTTCAGTCCCGTGGCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC 900
Qy 301 ProGlyAspCysProAsnPheAlaAlaProArgGluValAlaProProTyrGlnGly 320
Db 901 CCCGTTGACTTCCCACTTTGTGGCTCCCGCGACAGAGGTGGCACCACTATCAGGGG 960
Qy 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
Db 961 GCTGACCCCACTTTCGAGACAGCCCTCGCCCTCCGACCCCAATCCCAACCCCTTCAGAG 1020
Qy 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
Db 1021 TGGGAGGACACGCGCCCAAGCCACAGACCTAGACACTGATACCCCGCGACGCTGTAC 1080
Qy 361 AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeu 380
Db 1081 GCCGTGTGTGGAACAGTGTGCGCTGGGAGGAATTCGTGCGGCGCTCAGGGCTG 1140
Qy 381 SerAspHisGluIleAspArgLeuLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
Db 1141 AGCGACCAAGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCTCGCGGAGGCGCA 1200

Qy 401 TyrSerMetLeuAlaThrTyrArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420
Db 1201 TACAGCATGCTGGGACCTGGAGGGCGGCACCGCGCGGAGCCACCTGGAGCTG 1260
Qy 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
Db 1261 CTGGACACGCTGCTCCGCGACATGGACCTGCTGGGCTGCTGGAGGACATCGAGAGCG 1320
Qy 441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
Db 1321 CTTTGGCGCGCGCGCGCTCCCGCGCGCGCGCGCTCTCTCAGA 1365

RESULT 12

US-09-898-234-11
; Sequence 11, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: them
; FILE REFERENCE: 98,385-1
; CURRENT APPLICATION NUMBER: US/09/898,234
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (213)...(1325)
; OTHER INFORMATION: Description of Artificial Sequence: cDNA insert of
; OTHER INFORMATION: lambdaTNF-BP15 and pTNF-BP15 vectors
US-09-898-234-11

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 3,67e-207 | Length: | 1334 |
| Score: | 2069.00 | Matches: | 374 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 83.19% | Indels: | 0 |
| DB: | 9 | Gaps: | 0 |

US-09-899-422a-2 (1-455) x US-09-898-234-11 (1-1334)

Qy 1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuLeuVal 20
Db 213 ATGGCCCTCTCCACCGTCCCTGACCTGCTGCTGCACCTGGTCTCTGGAGCTGTGGTG 272
Qy 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
Db 273 GGAATATACCCCTCAGGGGTTATTGGACTGTGCTCCCTACCTAGGGGACAGGAGAGA 332
Qy 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
Db 333 GATAGTGTGTGCTCCCAAGGAATAATATATCCACCTCAAAATATTTCGATTGCTGTACC 392
Qy 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80

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Db 393 AAGTGCACAAAGAAACCTACTTGTACATGACTGTCCAGGCGCGGGGAGATACGGAC 452
QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
Db 453 TGCAGGAGGTGTGAGAGCGCTCTTCCAGCGTTCAGAAACACCTCAGACACTGCCCTC 512
QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluLeuSerSerCysThrValAsp 120
Db 513 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGTCTTCTTGCACAGTGGAC 572
QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
Db 573 CGGGACACCGTGTGTGGCTGCAGAGAACACCTACCGGCATTATTGGAGTGAACACCTT 632
QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
Db 633 TTCCACTGCTCAATTGCAGCTCTGCCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 692
QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
Db 693 AAACAGACACCGTGTGCACCTGCCATGCCATGAGGTCTTCTTCTAGAGAAACAGAGTGTGC 752
QY 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
Db 753 TCCGTGTAGTACTGTAGAAAGCCCTGGAGTGCAGCAAGTGTGCTACCCCAAGATGAG 812
QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
Db 813 AATGTTAAGGCACTCAGGACTCAGGCACACAGTGTGTGCCCTCGCTCATTTCTTT 872
QY 221 GlyLeuCysLeuLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
Db 873 GGTCTTTGCTTTTATCCCTCCCTTCATTGTTGTTATGTTATGCTATCCCAACGGTGAAG 932
QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGluLeuGlu 260
Db 933 TCCAACTCTACCTCCATTGTTGGGAAATCGACACCTCGAAAGAGGGGAGCTGAA 992
QY 261 GlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
Db 993 GGAACCTACTAAGCCCTGGCCCAACCCCAAGCTTCAGTCCCACTCCAGGCTTCACC 1052
QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrThr 300
Db 1053 CCACCTGGCTGTAGTCCGCTGCCAGTTCACCTTCACCTCCAGCTCCACCTATACC 1112
QY 301 ProGlyAspCysProAsnPheAlaProArgGluValAlaProProTyrGlnGly 320
Db 1113 CCGGTGTACTGTCCTCAACTTTCGCTCCCGCAGAGAGTGGCACCCCTATCAGGG 1172
QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
Db 1173 GCTGACCCCATCTTGCAGAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAAG 1232
QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
Db 1233 TGGGAGACAGCCGCCACAGCCACAGAGCGCTAGACACTGATGACCCCGGAGCGTATC 1292
QY 361 AlaValValGluAsnValProProLeuArgTyrIleLysGluPhe 374
Db 1293 GCCGTGGTGAGAACGTGCCCGCTGGCTGGAAGGAATTC 1334
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RESULT 13

US-09-792-356-11

; Sequence 11, Application US/09792356

; Publication No. US20020183485A1

; GENERAL INFORMATION:

; APPLICANT: Hauptmann, Rudolph

; APPLICANT: Himmler, Adolph

; APPLICANT: Maurer-Fogy, Ingrid

; APPLICANT: Stratowa, Christian

; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for

; TITLE OF INVENTION: Them

; FILE REFERENCE: 98,385-G

; CURRENT APPLICATION NUMBER: US/09/792,356

; PRIOR FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: 08/477,639

; PRIOR FILING DATE: 1995-06-07

; PRIOR APPLICATION NUMBER: 08/383,676

; PRIOR FILING DATE: 1995-02-01

; PRIOR APPLICATION NUMBER: 08/153,287

; PRIOR FILING DATE: 1993-11-17

; PRIOR APPLICATION NUMBER: 07/821,750

; PRIOR FILING DATE: 1992-01-02

; PRIOR APPLICATION NUMBER: 07/511,430

; NUMBER OF SEQ ID NOS: 87

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 11

; LENGTH: 1334

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (213)..(1325)

; OTHER INFORMATION: Description of Artificial Sequence: cDNA insert of

; OTHER INFORMATION: lambdaINF-BP15 and pINF-BP15 vectors

US-09-792-356-11

Alignment Scores:

Pred. No.: 3 67e-207 Length: 1334

Score: 2059.00 Matches: 374

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 83.19% Indels: 0

DB: 9 Gaps: 0

US-09-899-422a-2 (1-455) x US-09-792-356-11 (1-1334)

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QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
Db 273 GGAATATACCCCTCAGGGGTATTGGACTGTGCTCCTCACCCTCAGGGGACAGGAGAGA 332
QY 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 60
Db 333 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAAAATATTCGATTTGCTGTACC 392
QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
Db 393 AAGTGCACAAAGAAACCTACTTGTACAAATGACTGTCCAGGCGCGGGGAGGATACGGAC 452
QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
Db 453 TGCAGGAGGTGTGAGAGCGCTCTTCCAGCTTCAGAAACACCTCAGACACTGCCCTC 512
QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluLeuSerSerCysThrValAsp 120
Db 513 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGTCTTCTTGCACAGTGGAC 572
QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
Db 573 CGGGACACCGTGTGTGGCTGCAGAGAACACCTACCGGCATTATTGGAGTGAACACCTT 632
QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
Db 633 TTCCAGTGTCAATTGCAGCTCTGCCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 692
QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
Db 693 AAACAGACACCGTGTGAGAGCGCTCTTCTTCTAGAGAAACAGAGTGTGTGC 752
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QY 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
Db 753 TCCTGTAGTAACCTGTAAGAAAGCCCTGGAGTGCACGAAGTTGTGCTACCCAGATTGAG 812
QY 201 AsnValLysGlyThrGluAspSerGlyThrValLeuLeuProLeuValIlePhePhe 220
Db 813 AATGTTAAGGCACCTGAGGACTCAGCACACAGTGTGTGCTCCCTGGTCAATTTCTTT 872
QY 221 GlyLeuCysLeuLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
Db 873 GGTCTTTGCCCTTTATCCTCTCTTCATTTGTTAATGATCGCTACCAACGGTGGAG 932
QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGluLeuGlu 260
Db 933 TCCAAAGCTACTACCTCACTGTTGTGGAAATCGACACCTGAAAGAGGGGAGCTTCAA 992
QY 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
Db 993 GGAATCTACTAGACCCCTGGCCCCAAACCCAGCTTCAGTCCACCTCCAGGCTTACC 1052
QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrThrThr 300
Db 1053 CCCACCTCGGGCTTCAGTCCGCTGCCAGTTCACCTTCACCTCCAGCTCCACCTATACC 1112
QY 301 ProGlyAspCysProAsnPheAlaProArgArgGluValAlaProProThrGlnGly 320
Db 1113 CCCGGTGACTGTCACCACTTTGCGGCTCCCGSCAGAGAGTGGCACCACTATCAGGG 1172
QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
Db 1173 GCTGACCCCTTCCTTGCACAGCCCTCGCTCCGACCCCTCCCAACCCCTTCAGAG 1232
QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspProAlaThrLeuTyr 360
Db 1233 TGGGAGGACAGCCGCCACAGCCACAGAGCTAGACACTGATGACCCCGCAGCGTGAC 1292
QY 361 AlaValValGluAsnValProProLeuArgTrpLysGluPhe 374
Db 1293 GCGGTGGTGGAGAGCTGCCCGCTGCGCTGGGAAGGAATTC 1334

RESULT 14

US-09-899-422-11
; Sequence 11, Application US/09899422
; Patent No. US2002090676A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmeler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE OF INVENTION: them
; FILE REFERENCE: 98,385-H
; CURRENT APPLICATION NUMBER: US/09/899,422
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (213)..(1325)

; OTHER INFORMATION: Description of Artificial Sequence: cDNA insert of
; OTHER INFORMATION: lambdaTNF-BP15 and pTNF-BP15 vectors
US-09-899-422-11

Alignment Scores:

Pred. No.: 3,67e-207 Length: 1334
Score: 2069.00 Matches: 374
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.19% Indels: 0
DB: 10 Gaps: 0

US-09-899-422a-2 (1-455) x US-09-899-422-11 (1-1334)

QY 1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuGluLeuVal 20
Db 213 ATGGCCCTCTCCACCGTCCCTGACCTGCTGCTGCCACCTGGTCTCTCGAGCTGTGGTG 272
QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
Db 273 GGAATATACCCCTCAGGGGTATTGGACTGCTCCCTCACCTAGGGGACAGGAGAAGA 332
QY 41 AspSerValCysProGlnGlyLysThrIleHisProGlnAsnSerIleCysCysThr 60
Db 333 GATAGTGTGTGTCCTCCAAAGAAATATATCCACCTCAAAATAATTCGATTGCTGTACC 392
QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
Db 393 AAGTCCCAAAAGGAACCTACTGTACAACTGACTTCCAGGCCCGGGCAGATACGGAC 452
QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
Db 453 TGCAGGGAGTGTGAGAGCGGCTCTCTTCCACCGCTTCAGAAAAACCACTCAGACACTGCCTC 512
QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
Db 513 AGCTGCTCCAAATGCCGAAGAAATAGGTGAGTGGAGATCTCTTCTTGACAGTGGAC 572
QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
Db 573 CGGGACACCGTGTGTGGCTGCAGGAAGAACCACTACCGCATTTATGGAGTGAACCTT 632
QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
Db 633 TTCAGTGTCTTCAATTGCAGCTCTGCTCAATGGGACCGTGCACCTCTCTTCCAGGAG 692
QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
Db 693 AAACAGACACCGTGTGCACCTGCCATGACAGTTCTTCTTCTAAGAGAAAACAGTGTGTC 752
QY 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
Db 753 TCCGTAGTAACCTGTAAGAAAGCCCTGGAGTGCAGGAAGTTGTGCTACCCAGATTGAG 812
QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
Db 813 AATGTTAAGGCACCTGAGGACTCAGGCACACAGTGTGTGCTCCCTGGTCAATTTCTTT 872
QY 221 GlyLeuCysLeuLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
Db 873 GGTCTTTGCCCTTTATCCTCTCTTTCATTTGTTAATGATCGCTACCAACGGTGGAG 932
QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGluLeuGlu 260
Db 933 TCCAAAGCTACTACCTCACTGTTGTGGAAATCGACACCTGAAAGAGGGGAGCTTCAA 992
QY 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
Db 993 GGAATCTACTAGACCCCTGGCCCCAAACCCAGCTTCAGTCCACCTCCAGGCTTACC 1052
QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrThrThr 300
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